

141606

STIC-Biotech/ChemLib

From: Bunner, Bridget
Sent: Monday, January 03, 2005 12:49 PM
To: STIC-Biotech/ChemLib
Subject: sequence search

Hi! I'd like a sequence search performed for case 10/086,177:

1. the amino acid sequence of SEQ ID NO: 12
2. the amino acid sequence of SEQ ID NO: 13

CRAFE

Thanks!

Bridget Bunner

Art Unit 1647
Rem 4C65
(571) 272-0881
mailbox 4C70

STAFF USE ONLY

Searcher: _____
Searcher Phone: 2- _____
Date Searcher Picked up: 1/5/05
Date Completed: 1/5/05
Searcher Prep/Rev. Time: _____
Online Time: _____

Type of Search

NA Sequence: # _____
AA Sequence : # 2
Structure: # _____
Bibliographic: _____
Litigation: _____
Patent Family: _____
Other: _____

Vendors and cost where applicable

STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: QAP
WWW/Internet: _____
Other(Specify): _____

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 4, 2005, 15:43:59 ; Search time 27.3508 Seconds
(without alignments)
73.553 Million cell updates/sec

Title: US-10-086-177A-13

Perfect score: 175
Sequence: 1 KPVSLSYRCPCRFPGGGLKWIQIYLEKALN 31

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 478139 seqs, 6631800 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database:

Issued Patents AA:*

- 1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep:*
- 2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep:*
- 3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep:*
- 4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep:*
- 5: /cgn2_6/ptodata/1/1aa/PTCUS.COMB.pep:*
- 6: /cgn2_6/ptodata/1/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	167	95.4	31	4	US-09-543-940-5
2	155	88.6	27	4	US-09-543-940-4
3	132	75.4	25	4	US-09-543-940-6
4	123	70.3	27	4	US-09-543-940-7
5	117	66.9	89	1	US-08-181-556-2
6	117	66.9	89	1	US-08-323-084A-1
7	117	66.9	89	1	US-08-674-008-1
8	117	66.9	89	4	US-09-461-912A-46
9	117	66.9	93	1	US-08-323-084A-5
10	117	66.9	93	1	US-08-674-008-5
11	117	66.9	93	4	US-09-312-283C-421
12	117	66.9	93	4	US-09-919-497-95
13	117	66.9	166	4	US-09-646-028-5
14	117	66.9	177	4	US-09-646-028-54
15	117	66.9	326	3	US-08-808-720-3
16	117	66.9	326	4	US-09-467-638-3
17	117	66.9	328	3	US-08-808-720-1
18	117	66.9	328	4	US-09-467-638-1
19	117	66.9	339	4	US-09-646-028-55
20	82	46.9	14	4	US-09-543-940-10
21	69	39.4	13	4	US-09-543-940-9
22	62	35.4	10	4	US-09-543-940-8
23	61	34.9	1084	4	US-09-221-013A-8
24	60.5	34.6	974	4	US-08-960-048-6
25	60.5	34.6	974	4	US-08-838-586-6
26	58	33.1	535	4	US-09-252-991A-25662
27	57	32.6	97	4	US-09-270-767-39706

28	57	32.6	97	4	US-09-270-767-54923	Sequence 54923, A
29	57	32.6	192	4	US-09-270-767-32013	Sequence 32013, A
30	57	32.6	192	4	US-09-270-767-47230	Sequence 47230, A
31	56	32.0	701	4	US-09-248-796A-15250	Sequence 15250, A
32	55	31.4	10	4	US-09-543-940-12	Sequence 12, Appl
33	53	30.3	484	4	US-09-489-039A-9532	Sequence 9532, Ap
34	50	28.6	588	4	US-08-481-190-16	Sequence 16, Appl
35	50	28.6	588	5	PCT-US93-00869-16	Sequence 16, Appl
36	50	28.6	685	3	US-08-960-048-7	Sequence 7, Appl
37	50	28.6	685	4	US-09-838-586-7	Sequence 7, Appl
38	49.5	28.3	504	4	US-09-252-991A-32272	Sequence 32272, A
39	49	28.0	416	1	US-08-117-083-61	Sequence 61, Appl
40	49	28.0	488	4	US-08-311-731A-29	Sequence 29, Appl
41	48	27.4	78	3	US-09-188-930-158	Sequence 158, App
42	48	27.4	78	3	US-09-188-930-285	Sequence 285, App
43	48	27.4	78	4	US-09-312-283C-158	Sequence 158, App
44	48	27.4	78	4	US-09-312-283C-285	Sequence 285, App
45	48	27.4	125	3	US-08-722-126A-7	Sequence 7, Appl

ALIGNMENTS

```
RESULT 1
US-09-543-940-5
Sequence 5, Application US/09543940
Patent No. 6613742
GENERAL INFORMATION:
APPLICANT: Huang, Ziwei
APPLICANT: Luo, Zhaoen
APPLICANT: Zhou, Naiping
APPLICANT: Luo, Jiansong
TITLE OF INVENTION: Chemokine-Derived Synthetic Peptides
FILE REFERENCE: 8321-40
CURRENT APPLICATION NUMBER: US/09/543,940
PRIOR FILING DATE: 2000-04-06
PRIOR APPLICATION NUMBER: 60/128,106
PRIOR FILING DATE: 1999-04-07
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 5
LENGTH: 31
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURES:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: Peptide containing segments from N- and C-terminal
US-09-543-940-5

Query Match          95.4%; Score 167; DB 4; Length 31;
Best Local Similarity 96.8%; Pred. No. 5.2e-16;
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 KPVSLSYRCPCRFPGGGLKWIQIYLEKALN 31
DB      1 KPVSLSYRCPCRFPGGGLKWIQIYLEKALN 31

RESULT 2
US-09-543-940-4
Sequence 4, Application US/09543940
Patent No. 6613742
GENERAL INFORMATION:
APPLICANT: Huang, Ziwei
APPLICANT: Luo, Zhaoen
APPLICANT: Zhou, Naiping
APPLICANT: Luo, Jiansong
TITLE OF INVENTION: Chemokine-Derived Synthetic Peptides
FILE REFERENCE: 8321-40
CURRENT APPLICATION NUMBER: US/09/543,940
PRIOR FILING DATE: 2000-04-06
PRIOR APPLICATION NUMBER: 60/128,106
```

PRIOR FILING DATE: 1999-04-07
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 4
LENGTH: 27
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: peptide containing segments from N- and C-terminal
OTHER INFORMATION: regions of human SDF-1 protein
US-09-543-940-4

Query Match 88.6%; Score 155; DB 4; Length 27;
Best Local Similarity 100.0%; Pred. No. 1.9e-14;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 LSTRCPFRFGGGLKWIQIYLEKALN 31
DB 1 LSTRCPFRFGGGLKWIQIYLEKALN 27

RESULT 3
US-09-543-940-6
Sequence 6, Application US/09543940
Patent No. 6613742
GENERAL INFORMATION:
APPLICANT: Huang, Ziwel
APPLICANT: Luo, Zhaowen
APPLICANT: Zhou, Naiping
APPLICANT: Luo, Jiansong
TITLE OF INVENTION: Chemokine-Derived Synthetic Peptides
FILE REFERENCE: 8321-40
CURRENT APPLICATION NUMBER: US/09/543,940
CURRENT FILING DATE: 2000-04-06
PRIOR APPLICATION NUMBER: 60/128,106
PRIOR FILING DATE: 1999-04-07
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 6
LENGTH: 25
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: peptide containing segments from N- and C-terminal
OTHER INFORMATION: regions of human SDF-1 protein
US-09-543-940-6

Query Match 75.4%; Score 132; DB 4; Length 25;
Best Local Similarity 92.6%; Pred. No. 2.5e-11;
Matches 25; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

QY 5 LSTRCPFRFGGGLKWIQIYLEKALN 31
DB 1 LSTRCPFRFGGGLKWIQIYLEKALN 25

RESULT 4
US-09-543-940-7
Sequence 7, Application US/09543940
Patent No. 6613742
GENERAL INFORMATION:
APPLICANT: Huang, Ziwel
APPLICANT: Luo, Zhaowen
APPLICANT: Zhou, Naiping
APPLICANT: Luo, Jiansong
TITLE OF INVENTION: Chemokine-Derived Synthetic Peptides
FILE REFERENCE: 8321-40
CURRENT APPLICATION NUMBER: US/09/543,940
CURRENT FILING DATE: 2000-04-06
PRIOR APPLICATION NUMBER: 60/128,106
PRIOR FILING DATE: 1999-04-07

NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 7
LENGTH: 27
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: peptide containing segments from N- and C-terminal
OTHER INFORMATION: regions of human SDF-1 protein
US-09-543-940-7

Query Match 70.3%; Score 123; DB 4; Length 27;
Best Local Similarity 85.2%; Pred. No. 4.5e-10;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5 LSTRCPFRFGGGLKWIQIYLEKALN 31
DB 1 LSTRCPFRFGGGLKWIQIYLEKALN 27

RESULT 5
US-08-181-556-2
Sequence 2, Application US/08181556
Patent No. 5525486
GENERAL INFORMATION:
APPLICANT: HONJO, Tsauku
APPLICANT: TASHIRO, Kei
APPLICANT: TADA, Hideaki
TITLE OF INVENTION: PROCESS FOR CONSTRUCTING cDNA LIBRARY,
TITLE OF INVENTION: AND NOVEL POLYPEPTIDE AND DNA CODING FOR THE SAME
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSER: STEVENS, DAVIS, MILLER & MOSHER
STREET: 515 No. 5525486th Washington Street (P.O. Box 1427)
CITY: Alexandria
STATE: Virginia
COUNTRY: USA
ZIP: 22313
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/181,556
FILING DATE: 14-JAN-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 5-22098
FILING DATE: 14-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: POULOS III, James A.
REGISTRATION NUMBER: 31714
REFERENCE/DOCKET NUMBER: TPI/29088
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 549-7200
TELEFAX: (703) 528-5313
TELEX: 88-2746
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 89 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-181-556-2

Query Match 66.9%; Score 117; DB 1; Length 89;
Best Local Similarity 40.3%; Pred. No. 1e-08;
Matches 27; Conservative 0; Mismatches 4; Indels 36; Gaps 1;
QY 1 KPVSLSTRCPFRFGG-----GGLKWIQI 24
|||||

Db 22 KPVSLSTRCPREFSHVABANVHKLINTPNCALQIVARLKNRNQVCIDPRLKXIOE 81
 QY 25 YLEKALN 31
 |||||
 Db 82 YLEKALN 88

RESULT 6

US-08-323-084A-1
 ; Sequence 1, Application US/08323084A
 ; Patent No. 5563048
 ; GENERAL INFORMATION:
 ; APPLICANT: HONJO, TASHIKU
 ; APPLICANT: SHIROZU, MICHIO
 ; APPLICANT: TADA, HIDEAKI
 ; TITLE OF INVENTION: No. 5563048el Polypeptides and DNAs encoding them
 ; NUMBER OF SEQUENCES: 20
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS
 ; STREET: 2100 Pennsylvania Avenue, N.W.
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: U.S.A.
 ; ZIP: 20037-3202
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/323,084A
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: JP 280505/1993
 ; FILING DATE: 14-OCT-1993
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (202)293-7060
 ; TELEFAX: (202)293-7860
 ; TELEX: 6491103
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 89 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-323-084A-1

Query Match 66.9%; Score 117; DB 1; Length 89;

Best Local Similarity 40.3%; Pred. No. 1e-08;
 Matches 27; Conservative 0; Mismatches 4; Indels 36; Gaps 1;

QY 1 KPVSLSTRCPREFSHVABANVHKLINTPNCALQIVARLKNRNQVCIDPRLKXIOE 24
 |||||
 Db 22 KPVSLSTRCPREFSHVABANVHKLINTPNCALQIVARLKNRNQVCIDPRLKXIOE 81

QY 25 YLEKALN 31
 |||||
 Db 82 YLEKALN 88

RESULT 7

US-08-674-008-1
 ; Sequence 1, Application US/08674008
 ; Patent No. 5756084
 ; GENERAL INFORMATION:
 ; APPLICANT: HONJO, Tashiku
 ; APPLICANT: SHIROZU, Michio
 ; APPLICANT: TADA, Hideaki
 ; TITLE OF INVENTION: HUMAN STROMAL DERIVED
 ; FACTOR 1 AND 1 (As Amended)
 ; NUMBER OF SEQUENCES: 20
 ; CORRESPONDENCE ADDRESS:

ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS
 STREET: 2100 Pennsylvania Avenue, N.W.
 CITY: Washington
 STATE: D.C.
 COUNTRY: U.S.A.
 ZIP: 20037-3202

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/674,008
 ; FILING DATE: 1-JUL-1996
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/323,084
 ; FILING DATE: 14-OCT-1994
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: JP 280505/1993
 ; FILING DATE: 14-OCT-1993
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (202)293-7060
 ; TELEFAX: (202)293-7860
 ; TELEX: 6491103
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 89 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-674-008-1

Query Match 66.9%; Score 117; DB 1; Length 89;

Best Local Similarity 40.3%; Pred. No. 1e-08;
 Matches 27; Conservative 0; Mismatches 4; Indels 36; Gaps 1;

QY 1 KPVSLSTRCPREFSHVABANVHKLINTPNCALQIVARLKNRNQVCIDPRLKXIOE 24
 |||||
 Db 22 KPVSLSTRCPREFSHVABANVHKLINTPNCALQIVARLKNRNQVCIDPRLKXIOE 81

QY 25 YLEKALN 31
 |||||
 Db 82 YLEKALN 88

RESULT 8

US-09-461-912A-46
 ; Sequence 46, Application US/09461912A
 ; Patent No. 6709855
 ; GENERAL INFORMATION:
 ; APPLICANT: Stanton, Lawrence A.
 ; APPLICANT: White, R. Tyler
 ; APPLICANT: Damm, Deborah L.
 ; APPLICANT: Lewicki, John A.
 ; TITLE OF INVENTION: Methods for detection and use of
 ; FILE REFERENCE: SCIOS.011A
 ; CURRENT APPLICATION NUMBER: US/09/461,912A
 ; CURRENT FILING DATE: 1999-12-15
 ; PRIOR APPLICATION NUMBER: US 60/113,008
 ; PRIOR FILING DATE: 1998-12-18
 ; NUMBER OF SEQ ID NOS: 48
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 46
 ; LENGTH: 89
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-461-912A-46

Query Match 66.9%; Score 117; DB 4; Length 89;

Best Local Similarity 40.3%; Pred. No. 1e-08;
 Matches 27; Conservative 0; Mismatches 4; Indels 36; Gaps 1;

QY 1 KPVSLSYRCPCRFPGG-----GSLKXIOE 24
|||
DB 22 KPVSLSYRCPCRFESHVARANYKHILNTPNCALQIVARLKNRRQVCIDPRLKXIOE 81
|||
QY 25 YLEKALN 31
|||
DB 82 YLEKALN 88

RESULT 9

US-08-323-084A-5
; Sequence 5, Application US/08323084A
; Patent No. 5563048
; GENERAL INFORMATION:
; APPLICANT: HONTO, TASIYU
; APPLICANT: SHIROZU, MICHIO
; APPLICANT: TADA, HIDEKI
; TITLE OF INVENTION: No. 5563048e1 Polypeptides and DNAs encoding them
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS
; STREET: 2100 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20037-3202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/323,084A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 280505/1993
; FILING DATE: 14-OCT-1993
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)293-7060
; TELEFAX: (202)293-7860
; TELEX: 6491103
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 93 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-323-084A-5

Query Match 66.9%; Score 117; DB 1; Length 93;

Best Local Similarity 40.3%; Pred. No. 1e-08; 4; Indels 36; Gaps 1;
Matches 27; Conservative 0; Mismatches

QY 1 KPVSLSYRCPCRFPGG-----GSLKXIOE 24
|||
DB 22 KPVSLSYRCPCRFESHVARANYKHILNTPNCALQIVARLKNRRQVCIDPRLKXIOE 81
|||

QY 25 YLEKALN 31
|||
DB 82 YLEKALN 88

RESULT 10

US-08-674-008-5
; Sequence 5, Application US/08674008
; Patent No. 5756084
; GENERAL INFORMATION:
; APPLICANT: HONTO, TASIYU
; APPLICANT: SHIROZU, MICHIO
; APPLICANT: TADA, HIDEKI
; TITLE OF INVENTION: HUMAN STROMAL DERIVED

; TITLE OF INVENTION: FACTOR 1' AND 1 (As Amended)
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS
; STREET: 2100 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20037-3202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/674,008
; FILING DATE: 1-JUL-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/323,084
; FILING DATE: 14-OCT-1994
; PRIOR APPLICATION DATA: JP 280505/1993
; APPLICATION NUMBER: JP 280505/1993
; FILING DATE: 14-OCT-1993
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)293-7060
; TELEFAX: (202)293-7860
; TELEX: 6491103
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 93 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-674-008-5

Query Match

66.9%; Score 117; DB 1; Length 93;
Best Local Similarity 40.3%; Pred. No. 1e-08;
Matches 27; Conservative 0; Mismatches 4; Indels 36; Gaps 1;

QY 1 KPVSLSYRCPCRFPGG-----GSLKXIOE 24
|||
DB 22 KPVSLSYRCPCRFESHVARANYKHILNTPNCALQIVARLKNRRQVCIDPRLKXIOE 81
|||

QY 25 YLEKALN 31
|||
DB 82 YLEKALN 88

RESULT 11

US-09-312-283C-421
; Sequence 421, Application US/09312283C
; Patent No. 6573095
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Strachan, Lorna
; APPLICANT: Sleeman, Matthew
; APPLICANT: Orniet, Rene
; APPLICANT: Murison, James G.
; APPLICANT: Kumble, Krishanand D.
; TITLE OF INVENTION: Compositions Isolated from Skin Cells
; FILE REFERENCE: 11000.1011c2
; CURRENT APPLICATION NUMBER: US/09/312,283C
; CURRENT FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 425
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 421
; LENGTH: 93
; TYPE: PRT
; ORGANISM: Mouse
; US-09-312-283C-421

Query Match	66.9%	Score 117;	DB 4;	Length 93;
Best Local Similarity	40.3%;	Pred. No. 1e-08;		
Matches 27; Conservative	0;	Mismatches 4;	Indels 36;	Gaps 1;

Dy 1 KPVSLSYRCPCRFFGG-----GGLKWIQ 24
Db 22 KPVLSYRCPCRFFESHIARAVVKKLILTPNCALQIVARKNNRRQCIDPKLKIQE 81

QY	25	YLEKALN	31
Db	82	YLEKALN	88

RESULT 12
US-09-919-497-95
Sequence 95, Application US/09919497

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? APPLICANT: Muller, George L.
? TITLE OF INVENTION: PROGNOSTIC CLASSIFICATION OF ENDOMETRIAL CANCER
? FILE REFERENCE: B0801/7225
? CURRENT APPLICATION NUMBER: US/09/919,497
? CURRENT FILING DATE: 2001-07-31
? PRIOR APPLICATION NUMBER: US 60/221,735
? PRIOR FILING DATE: 2000-07-31
? NUMBER OF SEQ ID NOS: 100
? SOFTWARE: PatentIn version 3.0
? SEQ ID NO 95
? LENGTH: 93
? TYPE: prt
? ORGANISM: Homo sapiens
? IS-09-919-497-95

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Query Match	66.9%	Score 117;	DB 4;	Length 93;
Best Local Similarity	40.3%;	Pred. No. 1e-08;		
Matches 27; Conservative	0;	Mismatches 4;	Indels 36;	Gaps 1;

QY 1 KPVSLSYRCPCRFFGG-----GGLKWIQE 24
 |||||
 Db 22 KPVLSYRCRCRFFESHVARAVYKHLKIINTPNCALQIVARLKNNNRQVCIDPKLKIQE 81
 |||||

Qy	25	YLEKALN	31
Db	82	YLEKALN	88

RESULT 13
US-09-646-028-5
; Sequence 5, Application US/09646028

```

? APPLICANT: Kwak, Larry
? APPLICANT: Biregyn, Arya
? TITLE OF INVENTION: METHODS AND COMPOSITIONS OF
? TITLE OF INVENTION: CHEMOKINE-TUMOR ANTIGEN FUSION PROTEINS AS CANCER VACCINES
? FILE REFERENCE: 14014.0316/P
? CURRENT APPLICATION NUMBER: US/09/646,028
? CURRENT FILING DATE: 2000-09-12
? PRIOR APPLICATION NUMBER: 60/077,745
? PRIOR FILING DATE: 1998-03-12
? NUMBER OF SEQ ID NOS: 57
? SOFTWARE: FastSeq for Windows Version 3.0
? SEQ ID NO 5
? LENGTH: 166
? TYPE: PR1
? ORGANISM: Artificial Sequence
? FEATURES:
? OTHER INFORMATION: Description of artificial sequence: /note=synthetic construct
? IS-09-646-028-5

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Query Match	66.9%	Score 117;	DB 4;	Length 166;
Best Local Similarity	40.3%	Pred. No. 1.9e-08;		
Matches 27; Conservative	0;	Mismatches 4;	Indels 36;	Gaps 1

[illegible]

QY	25	YLEKALN	31
Db	82	YLEKALN	88

RESULT 14
US-09-646-028-54
; Sequence 54, Application US/09646028

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? APPLICANT: Kwak, Larry
? APPLICANT: Bhiragm, Arva
? TITLE OF INVENTION: METHODS AND COMPOSITIONS OF
? TITLE OF INVENTION: CHEMOKINE-TUMOR ANTIGEN FUSION PROTEINS AS CANCER VACCINES
? PIR REFERENCE: 14014.0316/P
? CURRENT APPLICATION NUMBER: US/09/646,028
? CURRENT FILING DATE: 2000-09-12
? PRIOR APPLICATION NUMBER: 60/077,745
? PRIOR FILING DATE: 1998-03-12
? NUMBER OF SEQ ID NOS: 57
? SOFTWARE: FastSeq for Windows Version 3.0
? SEQ ID NO 54
? LENGTH: 177
? TYPE: PR1
? ORGANISM: Artificial Sequence
? FEATURES:
? OTHER INFORMATION: Description of artificial sequence:/note=synthetic construct
IS-09-646-028-54
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Query Match	66.9%	Score 117;	DB 4;	Length 177;
Best Local Similarity	40.3%;	Pred. No. 2e-08;		
Matches 27; Conservative	0;	Mismatches 4;	Indels 36;	Gaps 1;

Dy 1 KPVSLSYRCRCRFEGG-----GGJLKWIQE 24
Db 4 KPVSLSYRCRCRFFESHVARANVKHLKILNTPNCALQIVARLKNNRRQCIDPKLKWIQE 63

Qy	25	YLEKALN	31
Db	64	YLEKALN	70

RESULT 15
US-08-808-720-3
; Sequence 3, Application US/08808720

APPLICANT: Herrmann, Steve
 APPLICANT: Swanberg, Stephen
 TITLE OF INVENTION: CHEMICK POLYPEPTIDES CONTAINING
 TITLE OF INVENTION: CHEMICK DOMAINS
 NUMBER OF SEQUENCES: 10
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Genetics Institute, Inc.
 STREET: 87 Cambridgepark
 CITY: Cambridge
 STATE: MA
 COUNTRY: USA
 ZIP: 02140
 COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/808,720
 FILING DATE:
 CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:
NAME: Sprunger, Suzanne
REGISTRATION NUMBER: P-41,323
REFERENCE/DOCKET NUMBER: G15291
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8284
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 326 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-808-720-3

Query Match 66.9%; Score 117; DB 3; Length 326;
Best Local Similarity 40.3%; Pred. No. 3.7e-08;
Matches 27; Conservative 0; Mismatches 4; Indels 36; Gaps 1;

QY	1	KPVSLSYRCPCRFEGG-----GGLKWIQE	24
DB	20	KPVSLSYRCPCRFESHVAPANVYHKLINTPNCALQIVARLKNNNRQVCIDPELKIQE	79
QY	25	YLEKALN	31
DB	80	YLEKALN	86

Search completed: January 4, 2005, 15:47:50
Job time: 28.9508 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 4, 2005, 15:46:58 ; Search time 101.131 Seconds
(without alignments)
110.268 Million cell updates/sec

Title: US-10-086-177a-13

Perfect score: 175
Sequence: 1 KPVSLSYRCPFRFGGGLKMIQIEYLEKALN 31

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 1599051 seqs, 359727711 residues

Total number of hits satisfying chosen parameters: 1599051

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications AA:*

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- 10: /cgn2_6/ptodaca/1/pubppaa/US09C_PUBCOMB.pep:*
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- 15: /cgn2_6/ptodaca/1/pubppaa/US10C_PUBCOMB.pep:*
- 16: /cgn2_6/ptodaca/1/pubppaa/US10C_PUBCOMB.pep:*
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- 18: /cgn2_6/ptodaca/1/pubppaa/US11_NEW_PUB.pep:*
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- 20: /cgn2_6/ptodaca/1/pubppaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	175	100.0	31 9 US-09-835-107-13	Sequence 13, App1
2	175	100.0	31 9 US-09-835-107-15	Sequence 15, App1
3	175	100.0	31 9 US-09-835-107-20	Sequence 20, App1
4	175	100.0	31 9 US-09-835-107-21	Sequence 21, App1
5	175	100.0	31 9 US-09-835-107-22	Sequence 22, App1
6	175	100.0	31 9 US-09-835-107-23	Sequence 23, App1
7	175	100.0	31 9 US-09-835-107-26	Sequence 26, App1
8	175	100.0	31 9 US-09-835-107-27	Sequence 27, App1
9	175	100.0	31 14 US-10-086-177a-13	Sequence 13, App1
10	175	100.0	31 14 US-10-086-177a-15	Sequence 15, App1
11	175	100.0	31 14 US-10-086-177a-20	Sequence 20, App1
12	175	100.0	31 14 US-10-086-177a-21	Sequence 21, App1
13	175	100.0	31 14 US-10-086-177a-22	Sequence 22, App1

14	175	100.0	31 14 US-10-086-177a-23	Sequence 23, App1
15	175	100.0	31 14 US-10-086-177a-26	Sequence 26, App1
16	175	100.0	31 14 US-10-086-177a-27	Sequence 27, App1
17	172	98.3	31 9 US-09-835-107-24	Sequence 24, App1
18	172	98.3	31 9 US-09-835-107-25	Sequence 25, App1
19	172	98.3	31 14 US-10-086-177a-24	Sequence 24, App1
20	172	98.3	31 14 US-10-086-177a-25	Sequence 25, App1
21	166	94.9	31 9 US-09-852-424-74	Sequence 74, App1
22	166	94.9	31 9 US-09-852-424-122	Sequence 122, App1
23	166	94.9	31 9 US-09-852-424-124	Sequence 124, App1
24	166	94.9	31 9 US-09-852-424-133	Sequence 133, App1
25	166	94.9	31 9 US-09-852-424-134	Sequence 134, App1
26	166	94.9	31 9 US-09-852-424-135	Sequence 135, App1
27	163.5	93.4	34 9 US-09-835-107-17	Sequence 17, App1
28	163.5	93.4	34 9 US-09-835-107-19	Sequence 19, App1
29	163.5	93.4	34 14 US-10-086-177a-17	Sequence 17, App1
30	163.5	93.4	34 14 US-10-086-177a-19	Sequence 19, App1
31	162	92.6	31 9 US-09-852-424-95	Sequence 95, App1
32	161	92.0	31 9 US-09-852-424-79	Sequence 79, App1
33	161	92.0	31 9 US-09-852-424-94	Sequence 94, App1
34	160	91.4	31 9 US-09-852-424-97	Sequence 97, App1
35	159	90.9	31 9 US-09-852-424-78	Sequence 78, App1
36	159	90.9	31 9 US-09-852-424-81	Sequence 81, App1
37	158.5	90.6	30 9 US-09-835-107-12	Sequence 12, App1
38	158.5	90.6	30 9 US-09-835-107-14	Sequence 14, App1
39	158.5	90.6	30 14 US-10-086-177a-12	Sequence 12, App1
40	158.5	90.6	30 14 US-10-086-177a-14	Sequence 14, App1
41	156	89.1	31 9 US-09-852-424-96	Sequence 96, App1
42	156	89.1	31 9 US-09-852-424-80	Sequence 80, App1
43	156	89.1	33 9 US-09-835-107-16	Sequence 16, App1
44	156	89.1	33 9 US-09-835-107-18	Sequence 18, App1
45	156	89.1	33 14 US-10-086-177a-16	Sequence 16, App1

ALIGNMENTS

RESULT 1
US-09-835-107-13
Sequence 13, Application US/09835107
Patent No. US20020165123A1
GENERAL INFORMATION:
APPLICANT: Tudan, Christopher R.
APPLICANT: Mezouk, Ahmed
APPLICANT: Arab, Lakhdar
APPLICANT: Saxena, Geeta
APPLICANT: Eaves, Connie J.
APPLICANT: Cashman, Johanne
APPLICANT: Clark-Lewis
APPLICANT: Salati, Hassan
TITLE OF INVENTION: CXCR4 AGONIST TREATMENT OF HEMATOPOIETIC CELLS
FILE REFERENCE: SMAR012
CURRENT APPLICATION NUMBER: US/09/835,107
CURRENT FILING DATE: 2001-08-20
PRIOR APPLICATION NUMBER: CA 2,305,036
PRIOR FILING DATE: 2000-04-12
PRIOR APPLICATION NUMBER: US 60/232,425
PRIOR FILING DATE: 2000-09-14
PRIOR APPLICATION NUMBER: CA 2,335,109
PRIOR FILING DATE: 2001-02-23
NUMBER OF SEQ ID NOS: 34
SOFTWARE: Patentm Ver. 2.0
SEQ ID NO 13
LENGTH: 31
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: DOMAIN
LOCATION: (16..119)
OTHER INFORMATION: spacer monomers (such as the illustrated glycine
OTHER INFORMATION: G's) may be used in variable numbers, such as 2, 3
OTHER INFORMATION: or 4 glycines.
OTHER INFORMATION: Synthesised in Laboratory:

OTHER INFORMATION: SDF-1(1-14)-(G)4-SDF-1(55-67) acid; or CTCB0013
US-09-835-107-13

Query Match 100.0%; Score 175; DB 9; Length 31;
Best Local Similarity 100.0%; Pred. No. 2.5e-16;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPVSLSYRCPCRFPGGGGLKMWIOEYLEKALN 31
DB 1 KPVSLSYRCPCRFPGGGGLKMWIOEYLEKALN 31

RESULT 2

US-09-835-107-15
Sequence 15, Application US/09835107
Patent No. US20020165123A1

GENERAL INFORMATION:
APPLICANT: Tudan, Christopher R.
APPLICANT: Merzouk, Ahmed
APPLICANT: Arab, Lakhdar
APPLICANT: Saxena, Geeta
APPLICANT: Baves, Connie J.
APPLICANT: Cashman, Johanne
APPLICANT: Clark-Lewis
APPLICANT: Salari, Hassan
TITLE OF INVENTION: CXCR4 AGONIST TREATMENT OF HEMATOPOIETIC CELLS
FILE REFERENCE: SMAR012
CURRENT APPLICATION NUMBER: US/09/835,107
CURRENT FILING DATE: 2001-08-20
PRIOR APPLICATION NUMBER: CA 2,305,036
PRIOR FILING DATE: 2000-04-12
PRIOR APPLICATION NUMBER: US 60/232,425
PRIOR FILING DATE: 2000-09-14
PRIOR APPLICATION NUMBER: CA 2,335,109
PRIOR FILING DATE: 2001-02-23
SOFTWARE: PatentIn Ver. 2.0

LENGTH: 31
SEQ ID NO 15
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: DOMAIN
LOCATION: (15)..(18)
OTHER INFORMATION: spacer monomers (such as the illustrated glycine
OTHER INFORMATION: G's) may be used in variable numbers, such as 2, 3
OTHER INFORMATION: or 4 glycines.
OTHER INFORMATION: Synthesised in Laboratory:
OTHER INFORMATION: SDF-1(1-14)-(G)4-SDF-1(55-67) amide; or CTCB0017
NAME/KEY: MOD RES
LOCATION: (31)
OTHER INFORMATION: AMIDATION
US-09-835-107-15

Query Match 100.0%; Score 175; DB 9; Length 31;
Best Local Similarity 100.0%; Pred. No. 2.5e-16;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPVSLSYRCPCRFPGGGGLKMWIOEYLEKALN 31
DB 1 KPVSLSYRCPCRFPGGGGLKMWIOEYLEKALN 31

RESULT 3

US-09-835-107-20
Sequence 20, Application US/09835107
Patent No. US20020165123A1

GENERAL INFORMATION:
APPLICANT: Tudan, Christopher R.
APPLICANT: Merzouk, Ahmed
APPLICANT: Arab, Lakhdar
APPLICANT: Saxena, Geeta
APPLICANT: Baves, Connie J.

APPLICANT: Cashman, Johanne
APPLICANT: Clark-Lewis
APPLICANT: Salari, Hassan
TITLE OF INVENTION: CXCR4 AGONIST TREATMENT OF HEMATOPOIETIC CELLS
FILE REFERENCE: SMAR012
CURRENT APPLICATION NUMBER: US/09/835,107
CURRENT FILING DATE: 2001-08-20
PRIOR APPLICATION NUMBER: CA 2,305,036
PRIOR FILING DATE: 2000-04-12
PRIOR APPLICATION NUMBER: US 60/232,425
PRIOR FILING DATE: 2000-09-14
PRIOR APPLICATION NUMBER: CA 2,335,109
PRIOR FILING DATE: 2001-02-23
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 20
LENGTH: 31
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: DOMAIN
LOCATION: (15)..(18)
OTHER INFORMATION: spacer monomers (such as the illustrated glycine
OTHER INFORMATION: G's) may be used in variable numbers, such as 2, 3
OTHER INFORMATION: or 4 glycines.
NAME/KEY: DOMAIN
LOCATION: (24)..(28)
OTHER INFORMATION: Cyclized, for example glutamate (R) and lysine (K)
OTHER INFORMATION: residues may be joined by side chain cyclization
OTHER INFORMATION: using a lactam formation procedure.
OTHER INFORMATION: Synthesised in Laboratory:
OTHER INFORMATION: SDF-1(1-14)-(G)4-SDF(55-67)-E24/K28-cyclic acid
US-09-835-107-20

Query Match 100.0%; Score 175; DB 9; Length 31;
Best Local Similarity 100.0%; Pred. No. 2.5e-16;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPVSLSYRCPCRFPGGGGLKMWIOEYLEKALN 31
DB 1 KPVSLSYRCPCRFPGGGGLKMWIOEYLEKALN 31

RESULT 4

US-09-835-107-21
Sequence 21, Application US/09835107
Patent No. US20020165123A1

GENERAL INFORMATION:
APPLICANT: Tudan, Christopher R.
APPLICANT: Merzouk, Ahmed
APPLICANT: Arab, Lakhdar
APPLICANT: Saxena, Geeta
APPLICANT: Baves, Connie J.
APPLICANT: Cashman, Johanne
APPLICANT: Clark-Lewis
APPLICANT: Salari, Hassan
TITLE OF INVENTION: CXCR4 AGONIST TREATMENT OF HEMATOPOIETIC CELLS
FILE REFERENCE: SMAR012
CURRENT APPLICATION NUMBER: US/09/835,107
CURRENT FILING DATE: 2001-08-20
PRIOR APPLICATION NUMBER: CA 2,305,036
PRIOR FILING DATE: 2000-04-12
PRIOR APPLICATION NUMBER: US 60/232,425
PRIOR FILING DATE: 2000-09-14
PRIOR APPLICATION NUMBER: CA 2,335,109
PRIOR FILING DATE: 2001-02-23
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 21
LENGTH: 31
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:

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; NAME/KEY: DOMAIN
; LOCATION: (15)..(18)
; OTHER INFORMATION: spacer monomers (such as the illustrated glycine
; OTHER INFORMATION: G's) may be used in variable numbers, such as 2, 3
; OTHER INFORMATION: or 4 glycines.
; NAME/KEY: DOMAIN
; LOCATION: (20)..(24)
; OTHER INFORMATION: Cyclized, for example glutamate (E) and lysine (K)
; OTHER INFORMATION: residues may be joined by side chain cyclization
; OTHER INFORMATION: using a lactam formation.
; OTHER INFORMATION: Synthesised in laboratory.
; OTHER INFORMATION: SDF-1(1-14)-(G)4-SDF-1(55-67)-K20/B24-cyclic acid
US-09-835-107-21

Query Match          100.0%; Score 175; DB 9; Length 31;
Best Local Similarity 100.0%; Pred. No. 2.5e-16;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KPVSLSYRCRCRFFGGGGLKMIQIYLEKALN 31
DB      1 KPVSLSYRCRCRFFGGGGLKMIQIYLEKALN 31

RESULT 5
US-09-835-107-22
; Sequence 22, Application US/09835107
; Patent No. US20020165123A1
; GENERAL INFORMATION:
; APPLICANT: Tudan, Christopher R.
; APPLICANT: Merzouk, Ahmed
; APPLICANT: Arab, Lakhdar
; APPLICANT: Saxena, Geeta
; APPLICANT: Baves, Connie J.
; APPLICANT: Cashman, Johanne
; APPLICANT: Clark-Lewis
; APPLICANT: Salari, Hassan
; TITLE OF INVENTION: CXCR4 AGONIST TREATMENT OF HEMATOPOIETIC CELLS
; FILE REFERENCE: SMAR012
; CURRENT APPLICATION NUMBER: US/09/835,107
; PRIOR FILING DATE: 2001-08-20
; PRIOR APPLICATION NUMBER: CA 2,305,036
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/232,425
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: CA 2,335,109
; PRIOR FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 22
LENGTH: 31
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: DOMAIN
LOCATION: (15)..(18)
OTHER INFORMATION: spacer monomers (such as the illustrated glycine
OTHER INFORMATION: G's) may be used in variable numbers, such as 2, 3
OTHER INFORMATION: or 4 glycines.
NAME/KEY: DOMAIN
LOCATION: (24)..(28)
OTHER INFORMATION: Cyclized, for example (E) and lysine (K) residues
OTHER INFORMATION: may be joined by side chain cyclization using a
OTHER INFORMATION: lactam formation procedure.
OTHER INFORMATION: Synthesised in laboratory.
OTHER INFORMATION: SDF-1(1-14)-(G)4-SDF-1(55-67)-B24/K28-cyclic
OTHER INFORMATION: amide: or CTCB0022
NAME/KEY: MOD_RES
LOCATION: (31)
OTHER INFORMATION: AMIDATION
US-09-835-107-22

Query Match          100.0%; Score 175; DB 9; Length 31;
Best Local Similarity 100.0%; Pred. No. 2.5e-16;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KPVSLSYRCRCRFFGGGGLKMIQIYLEKALN 31
DB      1 KPVSLSYRCRCRFFGGGGLKMIQIYLEKALN 31

RESULT 6
US-09-835-107-23
; Sequence 23, Application US/09835107
; Patent No. US20020165123A1
; GENERAL INFORMATION:
; APPLICANT: Tudan, Christopher R.
; APPLICANT: Merzouk, Ahmed
; APPLICANT: Arab, Lakhdar
; APPLICANT: Saxena, Geeta
; APPLICANT: Baves, Connie J.
; APPLICANT: Cashman, Johanne
; APPLICANT: Clark-Lewis
; APPLICANT: Salari, Hassan
; TITLE OF INVENTION: CXCR4 AGONIST TREATMENT OF HEMATOPOIETIC CELLS
; FILE REFERENCE: SMAR012
; CURRENT APPLICATION NUMBER: US/09/835,107
; PRIOR FILING DATE: 2001-08-20
; PRIOR APPLICATION NUMBER: CA 2,305,036
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/232,425
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: CA 2,335,109
; PRIOR FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 23
LENGTH: 31
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: DOMAIN
LOCATION: (15)..(18)
OTHER INFORMATION: spacer monomers (such as the illustrated glycine
OTHER INFORMATION: G's) may be used in variable numbers, such as 2, 3
OTHER INFORMATION: or 4 glycines.
NAME/KEY: DOMAIN
LOCATION: (20)..(24)
OTHER INFORMATION: Cyclized, for example glutamate (E) and lysine
OTHER INFORMATION: (K) residues may be joined by side chain
OTHER INFORMATION: cyclization using a lactam formation procedure.
OTHER INFORMATION: Synthesised in laboratory.
OTHER INFORMATION: SDF-1(1-14)-(G)4-SDF-1(55-67)-K20/B24-cyclic
OTHER INFORMATION: amide: or CTCB0021
NAME/KEY: MOD_RES
LOCATION: (31)
OTHER INFORMATION: AMIDATION
US-09-835-107-23

Query Match          100.0%; Score 175; DB 9; Length 31;
Best Local Similarity 100.0%; Pred. No. 2.5e-16;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KPVSLSYRCRCRFFGGGGLKMIQIYLEKALN 31
DB      1 KPVSLSYRCRCRFFGGGGLKMIQIYLEKALN 31

RESULT 7
US-09-835-107-26
; Sequence 26, Application US/09835107
; Patent No. US20020165123A1
; GENERAL INFORMATION:
; APPLICANT: Tudan, Christopher R.
; APPLICANT: Merzouk, Ahmed
; APPLICANT: Arab, Lakhdar
; APPLICANT: Saxena, Geeta
```

```

Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KPVSLSYRCRCRFFGGGGLKMIQIYLEKALN 31
DB      1 KPVSLSYRCRCRFFGGGGLKMIQIYLEKALN 31

RESULT 6
US-09-835-107-23
; Sequence 23, Application US/09835107
; Patent No. US20020165123A1
; GENERAL INFORMATION:
; APPLICANT: Tudan, Christopher R.
; APPLICANT: Merzouk, Ahmed
; APPLICANT: Arab, Lakhdar
; APPLICANT: Saxena, Geeta
; APPLICANT: Baves, Connie J.
; APPLICANT: Cashman, Johanne
; APPLICANT: Clark-Lewis
; APPLICANT: Salari, Hassan
; TITLE OF INVENTION: CXCR4 AGONIST TREATMENT OF HEMATOPOIETIC CELLS
; FILE REFERENCE: SMAR012
; CURRENT APPLICATION NUMBER: US/09/835,107
; PRIOR FILING DATE: 2001-08-20
; PRIOR APPLICATION NUMBER: CA 2,305,036
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/232,425
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: CA 2,335,109
; PRIOR FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 23
LENGTH: 31
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: DOMAIN
LOCATION: (15)..(18)
OTHER INFORMATION: spacer monomers (such as the illustrated glycine
OTHER INFORMATION: G's) may be used in variable numbers, such as 2, 3
OTHER INFORMATION: or 4 glycines.
NAME/KEY: DOMAIN
LOCATION: (20)..(24)
OTHER INFORMATION: Cyclized, for example glutamate (E) and lysine
OTHER INFORMATION: (K) residues may be joined by side chain
OTHER INFORMATION: cyclization using a lactam formation procedure.
OTHER INFORMATION: Synthesised in laboratory.
OTHER INFORMATION: SDF-1(1-14)-(G)4-SDF-1(55-67)-K20/B24-cyclic
OTHER INFORMATION: amide: or CTCB0021
NAME/KEY: MOD_RES
LOCATION: (31)
OTHER INFORMATION: AMIDATION
US-09-835-107-23

Query Match          100.0%; Score 175; DB 9; Length 31;
Best Local Similarity 100.0%; Pred. No. 2.5e-16;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KPVSLSYRCRCRFFGGGGLKMIQIYLEKALN 31
DB      1 KPVSLSYRCRCRFFGGGGLKMIQIYLEKALN 31

RESULT 7
US-09-835-107-26
; Sequence 26, Application US/09835107
; Patent No. US20020165123A1
; GENERAL INFORMATION:
; APPLICANT: Tudan, Christopher R.
; APPLICANT: Merzouk, Ahmed
; APPLICANT: Arab, Lakhdar
; APPLICANT: Saxena, Geeta
```

```
/ APPLICANT: Baves, Connie J.
/ APPLICANT: Cashman, Johanne
/ APPLICANT: Clark-Lewis
/ APPLICANT: Salari, Hassan
/ TITLE OF INVENTION: CXCR4 AGONIST TREATMENT OF HEMATOPOIETIC CELLS
/ FILE REFERENCE: SMAR012
/ CURRENT APPLICATION NUMBER: US/09/835,107
/ PRIOR FILING DATE: 2001-08-20
/ PRIOR APPLICATION NUMBER: CA 2,305,036
/ PRIOR FILING DATE: 2000-04-12
/ PRIOR APPLICATION NUMBER: US 60/232,425
/ PRIOR FILING DATE: 2000-09-14
/ PRIOR APPLICATION NUMBER: CA 2,335,109
/ NUMBER OF SEQ ID NOS: 34
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 26
/ LENGTH: 31
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ NAME/KEY: DOMAIN
/ LOCATION: (15)..(18)
/ OTHER INFORMATION: spacer monomers (such as the illustrated glycine
/ OTHER INFORMATION: G's) may be used in variable numbers, such as 2, 3
/ NAME/KEY: DISULFID
/ LOCATION: (9)..(11)
/ OTHER INFORMATION: cysteine residues may for example be involved in
/ OTHER INFORMATION: bridge formation
/ OTHER INFORMATION: Synthesized in Laboratory:
/ OTHER INFORMATION: SDF-1(1-14) - (G)4-SDF-1(55-67) -C9/C11-cyclic acid
US-09-835-107-26

Query Match          100.0%; Score 175; DB 9; Length 31;
Best Local Similarity 100.0%; Pred. No.2.5e-16;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY
1 KPVSLSYRCPCRFPGGGGLKMIQIYLEKALN 31
1 KPVSLSYRCPCRFPGGGGLKMIQIYLEKALN 31
Db
1 KPVSLSYRCPCRFPGGGGLKMIQIYLEKALN 31

RESULT 8
US-09-835-107-27
/ Sequence 27, Application US/09835107
/ Patent No. US20020165123A1
/ GENERAL INFORMATION:
/ APPLICANT: Tudan, Christopher R.
/ APPLICANT: Merzouk, Ahmed
/ APPLICANT: Arab, Lakhdar
/ APPLICANT: Saxena, Geeta
/ APPLICANT: Baves, Connie J.
/ APPLICANT: Cashman, Johanne
/ APPLICANT: Clark-Lewis
/ APPLICANT: Salari, Hassan
/ TITLE OF INVENTION: CXCR4 AGONIST TREATMENT OF HEMATOPOIETIC CELLS
/ FILE REFERENCE: SMAR012
/ CURRENT APPLICATION NUMBER: US/09/835,107
/ PRIOR FILING DATE: 2001-08-20
/ PRIOR APPLICATION NUMBER: CA 2,305,036
/ PRIOR FILING DATE: 2000-04-12
/ PRIOR APPLICATION NUMBER: US 60/232,425
/ PRIOR FILING DATE: 2000-09-14
/ PRIOR APPLICATION NUMBER: CA 2,335,109
/ NUMBER OF SEQ ID NOS: 34
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 27
/ LENGTH: 31
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ NAME/KEY: Artificial Sequence
```

```
/ NAME/KEY: DOMAIN
/ LOCATION: (15)..(18)
/ OTHER INFORMATION: spacer monomers (such as the illustrated glycine
/ OTHER INFORMATION: G's) may be used in variable numbers, such as 2, 3
/ NAME/KEY: DISULFID
/ LOCATION: (9)..(11)
/ OTHER INFORMATION: Cysteine residues may for example be involved in
/ OTHER INFORMATION: bridge formation.
/ OTHER INFORMATION: Synthesized in Laboratory:
/ OTHER INFORMATION: SDF-1(1-14) - (G)4-SDF-1(55-67) -C9/C11-cyclic amide
/ NAME/KEY: MOD_RES
/ LOCATION: (31)
/ OTHER INFORMATION: AMIDATION
US-09-835-107-27

Query Match          100.0%; Score 175; DB 9; Length 31;
Best Local Similarity 100.0%; Pred. No.2.5e-16;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY
1 KPVSLSYRCPCRFPGGGGLKMIQIYLEKALN 31
1 KPVSLSYRCPCRFPGGGGLKMIQIYLEKALN 31
Db
1 KPVSLSYRCPCRFPGGGGLKMIQIYLEKALN 31

RESULT 9
US-10-086-177a-13
/ Sequence 13, Application US/10086177A
/ Patent No. US20030148940A1
/ GENERAL INFORMATION:
/ APPLICANT: Tudan, Christopher R.
/ APPLICANT: Merzouk, Ahmed
/ APPLICANT: Saxena, Geeta
/ APPLICANT: Baves, Connie J.
/ APPLICANT: Cashman, Johanne
/ APPLICANT: Clark-Lewis, Ian
/ APPLICANT: Salari, Hassan
/ TITLE OF INVENTION: CXCR4 Agonist Treatment of Hematopoietic
/ FILE REFERENCE: SMAR-012CIP
/ CURRENT APPLICATION NUMBER: US/10/086,177A
/ PRIOR FILING DATE: 2002-02-26
/ PRIOR APPLICATION NUMBER: 09/835,107
/ PRIOR FILING DATE: 2001-04-12
/ PRIOR APPLICATION NUMBER: 60/232,425
/ PRIOR FILING DATE: 2000-09-14
/ PRIOR APPLICATION NUMBER: CA 2,305,036
/ PRIOR FILING DATE: 2000-04-12
/ PRIOR APPLICATION NUMBER: CA 2,335,109
/ NUMBER OF SEQ ID NOS: 34
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 13
/ LENGTH: 31
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Synthesized in Laboratory: SDF-1 (1-14) - (G)
/ OTHER INFORMATION: 3-SDF-1 (55-67) acid; or CTCBE0013
US-10-086-177a-13

Query Match          100.0%; Score 175; DB 14; Length 31;
Best Local Similarity 100.0%; Pred. No.2.5e-16;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY
1 KPVSLSYRCPCRFPGGGGLKMIQIYLEKALN 31
1 KPVSLSYRCPCRFPGGGGLKMIQIYLEKALN 31
Db
1 KPVSLSYRCPCRFPGGGGLKMIQIYLEKALN 31

RESULT 10
US-10-086-177a-15
/ Sequence 15, Application US/10086177A
```



```
; Publication No. US20030148940A1
; GENERAL INFORMATION:
; APPLICANT: Tudan, Christopher R.
; APPLICANT: Merzouk, Ahmed
; APPLICANT: Saxena, Geeta
; APPLICANT: Baves, Connie J.
; APPLICANT: Cashman, Johanne
; APPLICANT: Clark-Lewis, Ian
; APPLICANT: Salari, Hassan
; TITLE OF INVENTION: CXCR Agonist Treatment of Hematopoietic
; FILE REFERENCE: SMAR-012CIP
; CURRENT APPLICATION NUMBER: US/10/086,177A
; CURRENT FILING DATE: 2002-02-26
; PRIOR APPLICATION NUMBER: 09/835,107
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/232,425
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: CA 2,305,036
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: CA 2,335,109
; PRIOR FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURES:
; OTHER INFORMATION: Synthesized in Laboratory: SDF-1 (1-14) - (G)
; OTHER INFORMATION: 3-SDF-1 (55-67) amide: or CTCCE0017
US-10-086-177A-15
```

```
Query Match      100.0%; Score 175; DB 14; Length 31;
Best Local Similarity 100.0%; Pred. No. 2.5e-16;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 KPVSLSYRCPCRFPGGGGLKMWIOEYLEKALN 31
DB 1 KPVSLSYRCPCRFPGGGGLKMWIOEYLEKALN 31
```

```
RESULT 11
US-10-086-177A-20
; Sequence 20, Application US/10086177A
; Publication No. US20030148940A1
; GENERAL INFORMATION:
; APPLICANT: Tudan, Christopher R.
; APPLICANT: Merzouk, Ahmed
; APPLICANT: Saxena, Geeta
; APPLICANT: Baves, Connie J.
; APPLICANT: Cashman, Johanne
; APPLICANT: Clark-Lewis, Ian
; APPLICANT: Salari, Hassan
; TITLE OF INVENTION: CXCR Agonist Treatment of Hematopoietic
; FILE REFERENCE: SMAR-012CIP
; CURRENT APPLICATION NUMBER: US/10/086,177A
; CURRENT FILING DATE: 2002-02-26
; PRIOR APPLICATION NUMBER: 09/835,107
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/232,425
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: CA 2,305,036
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: CA 2,335,109
; PRIOR FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Artificial Sequence
```

```
; FEATURE:
; OTHER INFORMATION: Synthesized in Laboratory: SDF-1 (1-14) - (G)
; OTHER INFORMATION: 4-SDF-1 (55-67) - E24/K28-cyclic acid
US-10-086-177A-20
```

```
Query Match      100.0%; Score 175; DB 14; Length 31;
Best Local Similarity 100.0%; Pred. No. 2.5e-16;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 KPVSLSYRCPCRFPGGGGLKMWIOEYLEKALN 31
DB 1 KPVSLSYRCPCRFPGGGGLKMWIOEYLEKALN 31
```

```
RESULT 12
US-10-086-177A-21
; Sequence 21, Application US/10086177A
; Publication No. US20030148940A1
; GENERAL INFORMATION:
; APPLICANT: Tudan, Christopher R.
; APPLICANT: Merzouk, Ahmed
; APPLICANT: Saxena, Geeta
; APPLICANT: Baves, Connie J.
; APPLICANT: Cashman, Johanne
; APPLICANT: Clark-Lewis, Ian
; APPLICANT: Salari, Hassan
; TITLE OF INVENTION: CXCR Agonist Treatment of Hematopoietic
; FILE REFERENCE: SMAR-012CIP
; CURRENT APPLICATION NUMBER: US/10/086,177A
; CURRENT FILING DATE: 2002-02-26
; PRIOR APPLICATION NUMBER: 09/835,107
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/232,425
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: CA 2,305,036
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: CA 2,335,109
; PRIOR FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURES:
; OTHER INFORMATION: Synthesized in Laboratory: SDF-1 (1-14) - (G)
; OTHER INFORMATION: 4-SDF-1 (55-67) - K20/E24-cyclic acid
US-10-086-177A-21
```

```
Query Match      100.0%; Score 175; DB 14; Length 31;
Best Local Similarity 100.0%; Pred. No. 2.5e-16;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 KPVSLSYRCPCRFPGGGGLKMWIOEYLEKALN 31
DB 1 KPVSLSYRCPCRFPGGGGLKMWIOEYLEKALN 31
```

```
RESULT 13
US-10-086-177A-22
; Sequence 22, Application US/10086177A
; Publication No. US20030148940A1
; GENERAL INFORMATION:
; APPLICANT: Tudan, Christopher R.
; APPLICANT: Merzouk, Ahmed
; APPLICANT: Saxena, Geeta
; APPLICANT: Baves, Connie J.
; APPLICANT: Cashman, Johanne
; APPLICANT: Clark-Lewis, Ian
; APPLICANT: Salari, Hassan
; TITLE OF INVENTION: CXCR Agonist Treatment of Hematopoietic
; FILE REFERENCE: SMAR-012CIP
; CURRENT APPLICATION NUMBER: US/10/086,177A
; CURRENT FILING DATE: 2002-02-26
; PRIOR APPLICATION NUMBER: 09/835,107
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/232,425
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: CA 2,305,036
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: CA 2,335,109
; PRIOR FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Artificial Sequence
```

```
FILE REFERENCE: SMAR-012CIP
CURRENT APPLICATION NUMBER: US/10/086,177A
CURRENT FILING DATE: 2002-02-26
PRIOR APPLICATION NUMBER: 09/835,107
PRIOR FILING DATE: 2001-04-12
PRIOR APPLICATION NUMBER: 60/232,425
PRIOR FILING DATE: 2000-09-14
PRIOR APPLICATION NUMBER: CA 2,305,036
PRIOR FILING DATE: 2000-04-12
PRIOR APPLICATION NUMBER: CA 2,335,109
PRIOR FILING DATE: 2001-02-23
NUMBER OF SEQ ID NOS: 34
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 22
LENGTH: 31
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthesized in Laboratory: SDF-1 (1-14) - (G)
OTHER INFORMATION: 4-SDF-1 (55-67) - E24/K28-cyclic acid: or CTC0022
US-10-086-177A-22
```

```
Query Match          100.0%; Score 175; DB 14; Length 31;
Best Local Similarity 100.0%; Pred. No. 2.5e-16;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1 KPVSLSYRCPCRFPGGGGLKMIQIYELEKALN 31
Db 1 KPVSLSYRCPCRFPGGGGLKMIQIYELEKALN 31
```

```
RESULT 14
US-10-086-177A-23
Sequence 23; Application US/10086177A
Publication No. US20030148940A1
GENERAL INFORMATION:
APPLICANT: Tudan, Christopher R.
APPLICANT: Merzouk, Ahmed
APPLICANT: Saxena, Geeta
APPLICANT: Eaves, Connie J.
APPLICANT: Cashman, Johanne
APPLICANT: Clark-Lewis, Ian
APPLICANT: Salari, Hassan
TITLE OF INVENTION: CXCR Agonist Treatment of Hematopoietic
FILE REFERENCE: SMAR-012CIP
CURRENT APPLICATION NUMBER: US/10/086,177A
CURRENT FILING DATE: 2002-02-26
PRIOR APPLICATION NUMBER: 09/835,107
PRIOR FILING DATE: 2001-04-12
PRIOR APPLICATION NUMBER: 60/232,425
PRIOR FILING DATE: 2000-09-14
PRIOR APPLICATION NUMBER: CA 2,305,036
PRIOR FILING DATE: 2000-04-12
PRIOR APPLICATION NUMBER: CA 2,335,109
PRIOR FILING DATE: 2001-02-23
NUMBER OF SEQ ID NOS: 34
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 23
LENGTH: 31
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthesized in Laboratory: SDF-1 (1-14) - (G)
OTHER INFORMATION: 4-SDF-1 (55-67) - K20/E24-cyclic acid: or CTC0021
US-10-086-177A-23
```

```
Query Match          100.0%; Score 175; DB 14; Length 31;
Best Local Similarity 100.0%; Pred. No. 2.5e-16;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1 KPVSLSYRCPCRFPGGGGLKMIQIYELEKALN 31
Db 1 KPVSLSYRCPCRFPGGGGLKMIQIYELEKALN 31
```

```
Db 1 KPVSLSYRCPCRFPGGGGLKMIQIYELEKALN 31
```

```
RESULT 15
US-10-086-177A-26
Sequence 26; Application US/10086177A
Publication No. US20030148940A1
GENERAL INFORMATION:
APPLICANT: Tudan, Christopher R.
APPLICANT: Merzouk, Ahmed
APPLICANT: Saxena, Geeta
APPLICANT: Eaves, Connie J.
APPLICANT: Cashman, Johanne
APPLICANT: Clark-Lewis, Ian
APPLICANT: Salari, Hassan
TITLE OF INVENTION: CXCR Agonist Treatment of Hematopoietic
FILE REFERENCE: SMAR-012CIP
CURRENT APPLICATION NUMBER: US/10/086,177A
CURRENT FILING DATE: 2002-02-26
PRIOR APPLICATION NUMBER: 09/835,107
PRIOR FILING DATE: 2001-04-12
PRIOR APPLICATION NUMBER: 60/232,425
PRIOR FILING DATE: 2000-09-14
PRIOR APPLICATION NUMBER: CA 2,305,036
PRIOR FILING DATE: 2000-04-12
PRIOR APPLICATION NUMBER: CA 2,335,109
PRIOR FILING DATE: 2001-02-23
NUMBER OF SEQ ID NOS: 34
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 26
LENGTH: 31
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthesized in Laboratory: SDF-1 (1-14) - (G)
OTHER INFORMATION: 4-SDF-1 (55-67) - C9/C11-cyclic acid
US-10-086-177A-26
```

```
Query Match          100.0%; Score 175; DB 14; Length 31;
Best Local Similarity 100.0%; Pred. No. 2.5e-16;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1 KPVSLSYRCPCRFPGGGGLKMIQIYELEKALN 31
Db 1 KPVSLSYRCPCRFPGGGGLKMIQIYELEKALN 31
```

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Search completed: January 4, 2005, 16:05:00
Job time : 102.131 secs
```

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 4, 2005, 15:43:59 ; Search time 12.7049 Seconds
(without alignments)
234.769 Million cell updates/sec

Title: US-10-086-177A-13

Perfect score: 175
Sequence: 1 KPVSLSTRCPFRFFGGGGLKMWIGYLEKALN 31

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:*
1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	117	66.9	89	2	I53416 Interleukin-8 Homo
2	117	66.9	89	2	A53497 pre-B-cell growth-
3	117	66.9	93	2	G01540 cytokine SDF-1-bet
4	117	66.9	93	2	I81182 cytokine - mouse
5	61	34.9	1084	2	T08583 cellulose synthase
6	61	34.9	1088	2	H84604 probable cellulose
7	60.5	34.6	974	2	T10797 cellulose synthase
8	58	33.1	469	2	C83345 probable class III
9	58	33.1	1081	2	T52028 cellulose synthase
10	56	32.0	233	2	T35594 hypotetical prote
11	54	30.9	398	2	T52311 isopenicillin N ep
12	53	30.3	454	2	C64104 gamma-aminobutyric
13	53	30.3	470	2	T46814 gamma-aminobutyric
14	53	30.3	470	2	B95419 diaminobutyrate-py
15	50	28.6	202	2	A13489 cytochrome c-552 [
16	50	28.6	588	2	S34786 catechol oxidase (
17	50	28.6	685	2	T10800 cellulose synthase
18	49.5	28.3	170	2	B85359 hypotetical prote
19	49.5	28.3	577	2	I50731 Ig heavy chain - n
20	49	28.0	386	2	C81419 probable type IIS
21	49	28.0	517	2	F87198 glycerol kinase [i
22	49	28.0	517	2	A70793 probable glycerol
23	49	28.0	556	1	A53376 tryptophan 2-mono
24	49	28.0	557	1	A53493 tryptophan 2-mono
25	49	28.0	1722	2	A88470 protein C28H8.3 [i
26	48	27.4	189	2	D69389 DNA-directed RNA P
27	48	27.4	309	1	S34188 IGF PC receptor II
28	48	27.4	331	1	LNMSER IGF PC receptor, 1
29	48	27.4	383	2	C90136 26S proteasome SU

30	48	27.4	593	2	S30958 gene 13 protein -
31	48	27.4	661	2	S45131 probable membrane
32	48	27.4	1016	2	F82159 transpore, Acrb/
33	48	27.4	1429	2	S06434 homeotic protein 1
34	47.5	27.1	439	2	E32298 hypotetical prote
35	47.5	27.1	722	2	H96986 endo-1,4-beta gluc
36	47	26.9	203	2	I50481 synapse protein SN
37	47	26.9	358	2	S30901 isopenicillin N ep
38	47	26.9	409	2	S01825 transforming growt
39	47	26.9	623	2	T40685 phosphatidylcholin
40	47	26.9	1108	2	T35827 hypotetical prote
41	47	26.9	1400	2	T22644 hypotetical prote
42	46.5	26.6	1112	2	D96753 similar to disease
43	46.5	26.6	1287	2	T22235 hypotetical prote
44	46	26.3	122	2	T45165 succinate dehydrog
45	46	26.3	212	2	S73466 probable DNA prima

ALIGNMENTS

```

RESULT 1
I53416
Interleukin-8 homolog - mouse
C/Species: Mus sp. (mouse)
C/Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 05-Nov-1999
C/Accession: I53416
R/Jiang, W.; Zhou, P.; Kahn, S.M.; Tomita, N.; Johnson, M.D.; Weinstein, I.B.
Exp. Cell Res. 215, 284-293, 1994
A/Title: Molecular cloning of TP41, a gene whose expression is repressed by the tumor
A/Reference number: I53416, MUID:95073497, PMID:7982471
A/Accession: I53416
A/Status: preliminary; translated from GB/EMBL/DBDUT
A/Molecule type: mRNA
A/Residues: 1-89 <RES>
A/Cross-references: GB:574318; NID:9786393; PIDN:AA832650.1; PID:9786394
C/Genetic:
A/Gene: TP41
C/Superfamily: beta-chromoglobulin

Query Match      66.9%; Score 117; DB 2; Length 89;
Best Local Similarity 40.3%; Pred. No. 5.4e-09;
Matches 27; Conservative 0; Mismatches 4; Indels 36; Gaps 1;

QY      1 KPVSLSTRCPFRFFGG-----GGLKMWIG 24
      |||
Db      22 KPVSLSTRCPFRFFGGHARANYGHLKILNTPNCALQIVARLKNNNRQCIDPLKMWIG 81
      |||

QY      25 YLEKALN 31
      |||
Db      82 YLEKALN 88

RESULT 2
A53497
pre-B-cell growth-stimulating factor precursor - mouse
C/Species: Mus musculus (house mouse)
C/Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 09-Jul-2004
C/Accession: A53497, I59582
R/Nagasaki, T.; Kikuchi, H.; Kishimoto, T.
Proc. Natl. Acad. Sci. U.S.A. 91, 2305-2309, 1994
A/Title: Molecular cloning and structure of a pre-B-cell growth-stimulating factor.
A/Reference number: A53497, MUID:94181581, PMID:8134392
A/Accession: A53497
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-89 <NAG>
A/Cross-references: UNIPROT:P40224; GB:D21072; NID:9413905; PIDN:BA04648.1; PID:946845
R/Tashiro, K.; Tada, H.; Heliker, R.; Shioto, M.; Nakano, T.; Honjo, T.
Science 261, 600-603, 1993
A/Title: Signal sequence trap: a cloning strategy for secreted proteins and type I memb
A/Reference number: I59582, MUID:93342488, PMID:8342023
A/Accession: I59582

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A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-89 <RES>
A/Cross-references: GB:LI2029, NID:g393119, PIDN:AAA40100.1, PID:g393180
C/Genetics:
A:Gene: SDF-1-alpha
C/Superfamily: beta-chromoglobulin
C/Keywords: cytokine

Query Match 66.9%; Score 117; DB 2; Length 89;
Best Local Similarity 40.3%; Pred. No. 5.4e-09;
Matches 27; Conservative 0; Mismatches 4; Indels 36; Gaps 1;

QY 1 KPVSLSYRCPCRFPGG-----GGLKXIOE 24
DB 22 KPVSLSYRCPCRFPGSHIARANYKHLKILNTPNCALQIVARLKNNNRQVCIDPKLXIOE 81
QY 25 YLEKALN 31
DB 82 YLEKALN 88

RESULT 3
G01540
cytokine SDF-1-beta - human
C/Species: Homo sapiens (man)
C/Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 09-Jul-2004
C/Accession: G01540
R/Spotila, L.D.
submitted to the EMBL Data Library, October 1994
A/Reference number: G07697
A/Accession: G01540
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-93 <SPO>
A/Cross-references: UNIPROT:P48061, EMBL:U16752, NID:g1272194, PID:G571508
C/Superfamily: beta-chromoglobulin

Query Match 66.9%; Score 117; DB 2; Length 93;
Best Local Similarity 40.3%; Pred. No. 5.7e-09;
Matches 27; Conservative 0; Mismatches 4; Indels 36; Gaps 1;

QY 1 KPVSLSYRCPCRFPGG-----GGLKXIOE 24
DB 22 KPVSLSYRCPCRFPGSHIARANYKHLKILNTPNCALQIVARLKNNNRQVCIDPKLXIOE 81
QY 25 YLEKALN 31
DB 82 YLEKALN 88

RESULT 4
181182
cytokine - mouse
C/Species: Mus musculus (house mouse)
C/Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 09-Jul-2004
C/Accession: 181182
R/Tashiro, K.; Tada, H.; Heilker, R.; Shirozu, M.; Nakano, T.; Honjo, T.
Science 261, 600-603, 1993
A/Title: Signal sequence trap: a cloning strategy for secreted proteins and type I membr
A/Reference number: 159582; MUID:93342488; PMID:8342023
A/Accession: 181182
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-93 <RES>
A/Cross-references: UNIPROT:P40224; GB:LI2030, NID:g393181, PIDN:AAA40101.1, PID:g393182
C/Genetics:
A:Gene: SDF-1-beta
C/Superfamily: beta-chromoglobulin

Query Match 66.9%; Score 117; DB 2; Length 93;
Best Local Similarity 40.3%; Pred. No. 5.7e-09;
Matches 27; Conservative 0; Mismatches 4; Indels 36; Gaps 1;

QY 1 KPVSLSYRCPCRFPGG-----GGLKXIOE 24
DB 22 KPVSLSYRCPCRFPGSHIARANYKHLKILNTPNCALQIVARLKNNNRQVCIDPKLXIOE 81
QY 25 YLEKALN 31
DB 82 YLEKALN 88

RESULT 5

cellulose synthase (EC 2.4.1.-) catalytic chain - Arabidopsis thaliana
N/Alternate names: protein T22F8.250
C/Species: Arabidopsis thaliana (mouse-ear cress)
C/Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C/Accession: T08583; T09014
R/Bevan, M.; Zimmermann, W.; Gruenleisen, A.; Wambutt, R.; Bancroft, I.; Newes, H.W.; Ma,
submitted to the Protein Sequence Database, May 1999
A/Reference number: Z16442
A/Accession: T08583

A:Molecule type: DNA
A:Residues: 1-1084 <BEV>
A/Cross-references: UNIPROT:Q48947; EMBL:AL050351, GSPDB:GN00062; ATSP:T22F8.250
A/Experimental source: cultivar Columbia; BAC clone T22F8
R/Arifol, T.; Peng, L.; Betzner, A.S.; Burn, J.; Wiltke, W.; Herth, W.; Camilleri, C.;
Science 279, 717-720, 1998
A/Title: Molecular analysis of cellulose biosynthesis in Arabidopsis.
A/Reference number: Z13745; MUID:9811412; PMID:9445479
A/Accession: T09014
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1084 <ARI>
A/Cross-references: EMBL:AR027173, NID:g2827140; PIDN:AC39335.1; PID:g2827141
A/Experimental source: cultivar Columbia
C/Genetics:
A:Gene: ATSP:T22F8.250; Ath-A
A/Map position: 4
A/Initons: 27/3; 156/3; 191/1; 254/2; 343/2; 458/3; 504/3; 546/3; 617/3; 708/1; 773/3;
C/Keywords: cell wall synthesis; glycosyltransferase; hexosyltransferase

Query Match 34.9%; Score 61; DB 2; Length 1084;
Best Local Similarity 43.5%; Pred. No. 2.8;
Matches 10; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

QY 3 VLSYRCPCRFPGGGLKXIOE 25
DB 833 IFLSRHCPIWYGYGGGLKLERF 855

RESULT 6

H84604
probable cellulose synthase catalytic subunit [imported] - Arabidopsis thaliana
C/Species: Arabidopsis thaliana (mouse-ear cress)
C/Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C/Accession: H84604
R/Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.F.; Bentso, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffett, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon, L.
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter,
Nature 402, 761-768, 1999
A/Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A/Reference number: A84420; MUID:20083487; PMID:10617197
A/Accession: H84604

A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1088 <STO>
A/Cross-references: UNIPROT:Q9J22; GB:AE002093, NID:g4417271; PIDN:AAD20396.1; GSPDB:GT
C/Genetics:
A:Gene: ATG21770
A/Map position: 2

Query Match 34.9%; Score 61; DB 2; Length 1088;
Best Local Similarity 43.5%; Pred. No. 2.8;

Matches 10; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

QY 3 VSLSYRCPFRFGGGLKMIQY 25

Db 837 IFLSRHCPIMYGGGGLKMLERF 859

RESULT 7

T10797

cellulose synthase (EC 2.4.1.-) catalytic chain ceta1 - upland cotton

C/Species: Gossypium hirsutum (upland cotton)

C/Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004

C/Accession: T10797

R/Pear, J.R.; Kawagoe, Y.; Schreckengost, M.B.; Delmer, D.P.; Stalker, D.M.

Proc. Natl. Acad. Sci. U.S.A. 93, 12637-12642, 1996

A/Title: Higher plants contain homologs of the bacterial ceta genes encoding the catalytic

A/Reference number: 217152; MUID:97057296; PMID:8901635

A/Accession: T10797

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-974 <PRA>

A/Cross-references: UNIPROT:P93155; EMBL:U58283; NID:g1706955; PIDN:AAB37766.1; PID:g170

A/Experimental source: strain Acala SU-2; fiber

C/Genetics:

A/Gene: ceta1

A/Function: involved in the synthesis of cellulose

C/Keywords: glycosyltransferase; hexosyltransferase

Query Match 34.6%; Score 60.5; DB 2; Length 974;

Best Local Similarity 54.5%; Pred. No. 3;

Matches 12; Conservative 3; Mismatches 6; Indels 1; Gaps 1;

QY 3 VSLSYRCPFRFGGGLKMIQ 23

Db 721 IFLSRHCPIMYGGGGLKMLQ 742

RESULT 8

probable class III aminotransferase PA2413 [imported] - Pseudomonas aeruginosa (strain F

C/Species: Pseudomonas aeruginosa

C/Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004

C/Accession: C83345

R/Stover, C.K.; Pham, X.Q.; Eryin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; B

adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Laddig, K.; Lim,

Lozy, S.; Olson, M.V.

Nature 406, 959-964, 2000

A/Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho

A/Reference number: A82950; MUID:20437337; PMID:10984043

A/Accession: C83345

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-469 <STO>

A/Cross-references: UNIPROT:Q91168; GB:AE004668; GB:AE004091; NID:g9948446; PIDN:AA0580

A/Experimental source: strain PA01

C/Genetics:

A/Gene: PA2413

Query Match 33.1%; Score 58; DB 2; Length 469;

Best Local Similarity 43.3%; Pred. No. 3.3;

Matches 13; Conservative 1; Mismatches 16; Indels 0; Gaps 0;

QY 2 PVLSYRCPFRFGGGLKMIQYLERKAN 31

Db 199 PYDYRCPFRFGGGLKMIQYLERKAN 228

RESULT 9

cellulose synthase [imported] - Arabidopsis thaliana (fragment)

C/Species: Arabidopsis thaliana (mouse-ear cress)

C/Date: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 09-Jul-2004

C/Accession: T52028

R/Joshi, C.

submitted to the EMBL Data Library, May 1998

A/Reference number: Z25890

A/Accession: T52028

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-1081 <DOS>

A/Cross-references: UNIPROT:O65338; EMBL:AF062485; PIDN:AA029067.1

Query Match 33.1%; Score 58; DB 2; Length 1081;

Best Local Similarity 47.6%; Pred. No. 7.2;

Matches 10; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 3 VSLSYRCPFRFGGGLKMIQ 23

Db 831 IFLSRHCPIMYGGGGLKMLERF 851

RESULT 10

hypothetical protein SC6G4.43c SC6G4.43c - Streptomyces coelicolor

C/Species: Streptomyces coelicolor

C/Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 09-Jul-2004

C/Accession: T35594

R/Saunders, D.; Harris, D.; Parkhill, J.; Barrall, B.G.; Rajandream, M.A.

submitted to the EMBL Data Library, August 1998

A/Reference number: Z21583

A/Accession: T35594

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-233 <SNV>

A/Cross-references: UNIPROT:O68804; EMBL:AL031317; PIDN:CAA20421.1; GSPDB:GN00070; SCOE

A/Experimental source: strain A3 (2)

C/Genetics:

A/Gene: SCOEDB:SC6G4.43c

C/Superfamily: hypothetical protein HI0278

Query Match 32.0%; Score 56; DB 2; Length 233;

Best Local Similarity 44.0%; Pred. No. 3.3;

Matches 11; Conservative 5; Mismatches 7; Indels 2; Gaps 1;

QY 6 SYRCPFRFGGGLKMIQYLERK 28

Db 135 SGRIKPTFGHMGSPRWKRWK 159

RESULT 11

isopenicillin N epimerase [validated] - Streptomyces clavuligerus

C/Species: Streptomyces clavuligerus

C/Date: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 09-Jul-2004

C/Accession: T52311

R/Kovacevic, S.; Tobin, M.B.; Miller, J.R.

J. Bacteriol. 172, 3952-3958, 1990

A/Title: The beta-lactam biosynthetic genes for isopenicillin N epimerase and desacetoxy

A/Reference number: Z26033; MUID:90299822; PMID:1694525

A/Accession: T52311

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-398 <KOV>

A/Cross-references: UNIPROT:P18549; EMBL:M32324; PIDN:AAA26714.1

C/Genetics:

A/Gene: cefD

Query Match 30.9%; Score 54; DB 2; Length 398;

Best Local Similarity 53.3%; Pred. No. 10;

Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 8 RCPFRFGGGLKMI 22

Db 205 RIPCDFVAGSGHKWL 219

RESULT 12

C64104

gamma-aminobutyrate aminotransferase (EC 2.6.1.-) - Haemophilus influenzae (strain Rd K)

C/Species: Haemophilus influenzae
C/Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 09-Jul-2004

C/Accession: C64104; JCS879

R/Fieldname: R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Keriavage, A.; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodet, A.; Kelley, J.M.; Weidman, J.

D.M.; Brandon, R.C.; Pine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.

Science 269, 496-512, 1995

A/Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A./Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.

A/Reference number: A64000; MUID:95350630; PMID:7542800

A/Accession: C64104

A/Status: nucleic acid sequence not shown; translation not shown

A/Molecule type: DNA

A/Residues: 1-454 <TKR>

A/Cross-references: UNIPROT:P44951; GB:U32776; GB:I42023; NID:g1573969; PIDN:AAC22610.1;

R/ikai, H.; Yamamoto, S.

Bio1. Pharm. Bull. 21, 170-173, 1998

A/Title: Two genes involved in the 1,3-diaminopropane production pathway in Haemophilus

A/Reference number: JCS879; MUID:96173550; PMID:9514614

A/Status: nucleic acid sequence not shown

A/Molecule type: DNA

A/Residues: 1-454 <TKR>

A/Cross-references: GB:U32776; NID:g1573969; PIDN:AAC22610.1; PID:g1573974

C/Comment: This enzyme is involved in the pathway of 1,3-diaminopropane synthesis.

C/Genetics:

A/Note: neither the complete nucleic acid sequence nor the complete translation are shown

C/Superfamily: beta-alanine-pyruvate transaminase

C/Keywords: aminotransferase; phosphoprotein; pyridoxal phosphate

F/287/Binding site: pyridoxal phosphate (lys) (covalent) #status predicted

Query Match 30.3%; Score 53; DB 2; Length 454;

Best Local Similarity 38.5%; Pred. No. 16;

Matches 10; Conservative 3; Mismatches 13; Indels 0; Gaps 0;

Query Match 30.3%; Score 53; DB 2; Length 454;

Best Local Similarity 38.5%; Pred. No. 16;

Matches 10; Conservative 3; Mismatches 13; Indels 0; Gaps 0;

Query Match 30.3%; Score 53; DB 2; Length 454;

Best Local Similarity 38.5%; Pred. No. 16;

Matches 10; Conservative 3; Mismatches 13; Indels 0; Gaps 0;

Query Match 30.3%; Score 53; DB 2; Length 454;

Best Local Similarity 38.5%; Pred. No. 16;

Matches 10; Conservative 3; Mismatches 13; Indels 0; Gaps 0;

Query Match 30.3%; Score 53; DB 2; Length 454;

Best Local Similarity 38.5%; Pred. No. 16;

Matches 10; Conservative 3; Mismatches 13; Indels 0; Gaps 0;

Db 198 PYPAYRCP---FGGNETATLAAYFERAL 226

RESULT 14

B95419

diaminobutyrate-pyruvate transaminase (EC 2.6.1.46) Rhba [imported] - Sinorhizobium meliloti

C/Species: Sinorhizobium meliloti
C/Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004

C/Accession: B95419

R/Barnett, M.J.; Fisher, R.F.; Jones, T.; Kemp, C.; Abola, A.P.; Barlow-Hubler, F.; Bowers,

C.; Kalman, S.; Keating, D.H.; Palm, C.; Beck, M.C.; Surzycki, R.; Wells, D.H.; Yen, K.C.

Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001

A/Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium meliloti

A/Reference number: A95262; MUID:21396509; PMID:1148132

A/Accession: B95419

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-470 <TKR>

A/Cross-references: UNIPROT:Q923R2; GB:AB06469; PIDN:AAK65916.1; PID:g14524429; GSPDB:G

R/Galbert, F.; Flinn, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barlow-Hubler,

Pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federpiet, N.A.; Fisher, R.F.,

L.; Hyman, R.W.; Jones, T.

Science 293, 668-672, 2001

A/Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kise, E.; Komp, C.; Lelaure,

hehault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K

A/Title: The composite genome of the legume symbiont Sinorhizobium meliloti.

A/Reference number: A96039; MUID:21368234; PMID:11474104

A/Contents: annotation

C/Genetics:

A/Genome: rhbA

A/Superfamily: beta-alanine-pyruvate transaminase

C/Keywords: aminotransferase

Query Match 30.3%; Score 53; DB 2; Length 470;

Best Local Similarity 43.8%; Pred. No. 16;

Matches 14; Conservative 2; Mismatches 10; Indels 6; Gaps 2;

Query Match 30.3%; Score 53; DB 2; Length 470;

Best Local Similarity 43.8%; Pred. No. 16;

Matches 14; Conservative 2; Mismatches 10; Indels 6; Gaps 2;

Query Match 30.3%; Score 53; DB 2; Length 470;

Best Local Similarity 43.8%; Pred. No. 16;

Matches 14; Conservative 2; Mismatches 10; Indels 6; Gaps 2;

Query Match 30.3%; Score 53; DB 2; Length 470;

Best Local Similarity 43.8%; Pred. No. 16;

Matches 14; Conservative 2; Mismatches 10; Indels 6; Gaps 2;

Query Match 30.3%; Score 53; DB 2; Length 470;

Best Local Similarity 43.8%; Pred. No. 16;

Matches 14; Conservative 2; Mismatches 10; Indels 6; Gaps 2;

Qy 6 SYRCPFRFGGGLXWIOEYLEKAL 30
Db 117 SYSAMKEFGAAGNKWDPEHLNKFL 141

Search completed: January 4, 2005, 15:44:33
Job time : 13.7049 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 4, 2005, 15:43:59 ; Search time 59.459 Seconds
(without alignments)
299.982 Million cell updates/sec

Title: US-10-086-177A-13
Perfect score: 175
Sequence: 1 KPVSLSYRCPCRFPGGGLKWKIQRYLEKALN 31

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues
Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt 02:.*
1: uniprot_sprot:.*
2: uniprot_trembl:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	117	66.9	89	1	SDP1_MOUSE
2	117	66.9	89	2	Q8H7FO
3	117	66.9	89	2	BAA28601
4	117	66.9	89	2	CAC10203
5	117	66.9	89	2	BAC32216
6	117	66.9	89	2	BAC35845
7	117	66.9	89	2	CAG29279
8	117	66.9	92	2	Q9H554
9	117	66.9	93	1	SDP1_FELCA
10	117	66.9	93	1	SDP1_HUMAN
11	117	66.9	116	2	Q6EKW4
12	117	66.9	137	2	Q80ZM4
13	116	66.3	89	2	Q6T7C0
14	116	66.3	89	2	AAR88102
15	116	66.3	89	2	AAR91695
16	116	66.3	131	2	Q6T7B9
17	116	66.3	131	2	AAR91696
18	114	65.1	89	2	Q9QZD1
19	114	65.1	119	2	Q80YV8
20	105	60.0	94	2	Q8UUY9
21	105	60.0	94	2	AAR61945
22	61	34.9	507	2	Q93YF8
23	61	34.9	1088	2	Q9S7J2
24	61	34.9	1088	2	Q9S7J2
25	60.5	34.6	974	2	Q8M1M0
26	60.5	34.6	974	2	Q8M1M0
27	60	34.3	1078	2	Q6UDF1
28	60	34.3	1078	2	AAR23310
29	59	33.7	1084	2	Q6GUG6
30	58	33.1	346	2	Q8L778
31	58	33.1	366	2	Q94JG6

32	58	33.1	460	2	Q6D4Z7	Q6D4Z7 erwina car
33	58	33.1	469	2	Q9T168	Q9T168 pseudomonas
34	58	33.1	1069	2	Q9F1B9	Q9F1B9 arabidopsis
35	58	33.1	1081	2	Q6S338	Q6S338 arabidopsis
36	58	33.1	1084	2	Q9F6P9	Q9F6P9 arabidopsis
37	58	33.1	1087	2	Q6XZC2	Q6XZC2 populus tre
38	58	33.1	1087	2	AAP40636	AAP40636 populus t
39	57.5	32.9	939	2	Q943H3	Q943H3 cryza bati
40	57	32.6	192	2	Q707H1	Q707H1 escherichia
41	57	32.6	192	2	CAE85184	CAE85184 escherich
42	57	32.6	199	2	Q7C009	Q7C009 shigella fl
43	57	32.6	199	2	Q83J00	Q83J00 shigella fl
44	57	32.6	199	2	Q8FRT6	Q8FRT6 escherichia
45	57	32.6	424	2	Q9VCS4	Q9VCS4 dtrosophila

ALIGNMENTS

RESULT 1	SDP1_MOUSE	STANDARD;	PRT;	89 AA.
AC	P40224;			
DT	01-FEB-1995 (Rel. 31, last sequence update)			
DT	01-FEB-1995 (Rel. 31, last sequence update)			
DT	01-OCT-2004 (Rel. 45, last annotation update)			
DE	Stromal cell-derived factor 1 precursor (SDP-1) (CXCL12) (pre-B cell growth stimulating factor) (PBSF) (12-O-tetradecanoylphorbol 13-acetate repressed protein 1) (TPAR1) (thymic lymphoma cell stimulating factor) (Tlspf).			
GN	Name=Cxcl12; Synonyms=Sdf1;			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.			
NCBI	Taxid=10090;			
RM	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=94181581; PubMed=8134392;			
RA	Nagasawa T., Kikuchi H., Kishimoto T.,			
RT	"Molecular cloning and structure of a pre-B-cell growth-stimulating factor."			
RL	Proc. Natl. Acad. Sci. U.S.A. 91:2305-2309(1994).			
RM	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=93342488; PubMed=8342023;			
RA	Taahiro K., Tada H., Heilker R., Shirozu M., Nakano T., Honjo T.,			
RT	"Signal sequence trap: a cloning strategy for secreted proteins and type I membrane proteins."			
RL	Science 261:600-603(1993).			
RM	[3]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=95073497; PubMed=7982471;			
RA	Jiang W., Zhou P., Kahn S.M., Tomita N., Johnson M.D., Weinstein I.B.,			
RT	"Molecular cloning of TPAP, a gene whose expression is repressed by the tumor promoter 12-O-tetradecanoylphorbol 13-acetate (TPA)."			
RL	Exp. Cell Res. 215:284-293(1994).			
RM	[4]			
RP	SEQUENCE FROM N.A.			
RX	STRAIN=AKR/J;			
RA	Nomura M., Nakata Y., Uzawa A., Nose M., Akashi M., Suzuki G.,			
RT	Submitted (DEC-1994) to the EMBL/GenBank/DBJ databases.			
RM	[5]			
RP	SEQUENCE FROM N.A. (ISOFORM ALPHA).			
RX	STRAIN=C57BL/6J; TISSUE=Kidney;			
RA	MEDLINE=22354683; PubMed=1246851; DOI=10.1038/nature01266;			
RT	Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,			
RL	Nikaido I., Osato N., Saito R., Suzuki H., Yamanka I., Kiyosawa H.,			
RA	Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schombach C., Gojodori T.,			
RA	Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,			
RA	Schirral L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,			
RA	Blake J.B., Brad D., Brusci V., Choitha C., Corbani L.E., Cousins S.,			
RA	Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazier K.S.,			
RA	Gaasterland T., Gariboldi M., Giasi C., Godzik A., Gough J.,			

RA Grilmond S., Guetincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
 RA Kanai A., Kawai H., Kawasaki Y., Kedzierski R.M., King B.L.,
 RA Kanagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
 RA Megliot D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
 RA Nagashima T., Numa K., Okido T., Pavan M.J., Petre G., Pesole G.,
 RA Petrovsky N., Pillai R., Pontus J.U., Qi D., Ramachandran S.,
 RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
 RA Sanderlin A., Schneider C., Semple C.A., Setou M., Shimada K.,
 RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
 RA Vercaro R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
 RA Wilming L.G., Wyszynski-Boris A., Yangisawa M., Yang I., Yang L.,
 RA Yuan Z., Zavalan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
 RA Hirozane-Kishikawa T., Kono H., Nakamura M., Sakazume N., Sato K.,
 RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
 RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
 RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
 RA Yamanishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
 RA Birney E., Hayashizaki Y.,
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs."
 RT Nature 420:563-573(2002).
 RL
 RP SEQUENCE FROM N.A. (ISOFORM ALPHA).
 RC STRAIN=C57BL/6J; TISSUE=Mammary gland;
 RX MEDLINE=23388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Straubeberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Datchenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,
 RA Saplinton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Uedlin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loguigliano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
 RA Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grilmond J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywiński M.I., Skalska U., Smallus D.E.,
 RA Scherch A., Schein J.B., Jones S.J.W., Maria M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -1- FUNCTION: Chemottractant active on T-lymphocytes, monocytes, but
 CC not neutrophils.
 CC -1- FUNCTION: Stimulates the proliferation of bone marrow-derived b
 CC progenitor cells in the presence of IL-7 as well as growth of the
 CC stromal cell-dependent B-cell clone DM34 cells.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named Isoforms=2;
 CC Name=Alpha;
 CC IsoId=P40224-1; Sequence=Displayed;
 CC Name=Beta;
 CC IsoId=P40224-2; Sequence=VSP_001057;
 CC -1- SIMILARITY: Belongs to the Interleukin alpha (chemokine CXC)
 CC family.
 CC -----
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 CC entities requires a license agreement (See <http://www.isb-bib.ch/announce/>
 CC or send an email to license@isb-bib.ch).
 CC -----
 CC EMBL; D21072; BAA04648.1; -
 CC EMBL; L12029; AAA040100.1; -
 CC EMBL; L12030; AAA040101.1; -
 CC EMBL; S74318; AAB32650.1; -
 CC EMBL; D43804; BAA07862.1; -

DR EMBL; D43805; BAA07863.1; -
 DR EMBL; AK075596; BAC35845.1; -
 DR EMBL; BC006640; AAB06640.1; -
 DR PIR; A53497; A53497.
 DR PIR; A53497; A53497.
 DR PIR; A53497; A53497.
 DR HSSP; P48061; ISDF.
 DR HSSP; P48061; ISDF.
 DR MGI; MGI:103556; Cxcl12.
 DR GO; GO:0008009; F:chemokine activity; IDA.
 DR GO; GO:0007420; P:brain development; IDA.
 DR GO; GO:0030334; P:regulation of cell migration; IDA.
 DR GO; GO:0030334; P:regulation of cell migration; IDA.
 DR InterPro; IPR002473; C-X-C/Interlkn_8.
 DR InterPro; IPR001811; Chemokine_IL8.
 DR InterPro; IPR001089; CXC_chemkine_eml1.
 DR Pfam; PF00048; IL8; 1.
 DR PRINTS; PR00436; INTERLEUKIN8.
 DR PROSITE; PS00471; SMALL_CYTOKINES_CXC; FALSE NEG.
 KW Alternative splicing; Chemotaxis; Cytokine; Growth factor; Signal.
 FT SIGNAL 1 21 potential.
 FT CHAIN 22 89 Stromal cell-derived factor 1.
 FT DISUPRID 30 55 By similarity.
 FT DISUPRID 32 71 By similarity.
 FT VARSPIC 89 K->KRLKK (in Isoform Beta).
 FT FTID=VSP_001057.
 SQ SEQUENCE 89 AA; 10032 MW; C4B8AD69078B55FA CRC64;
 Query Match 66.9%; Score 117; DB 1; Length 89;
 Best Local Similarity 40.3%; Pred. No. 6e-09;
 Matches 27; Conservative 0; Mismatches 4; Indels 36; Gaps 1;
 QY 1 KPVSLSYRCRCRFFGG-----GGLKRWIOE 24
 Db 22 KPVSLSYRCRCRFFGGHIANVGHILINTPNCALQIVARLKNRRVCIDPKLKWIOE 81
 QY 25 YLEKALN 31
 Db 82 YLEKALN 88
 RESULT 2
 ID Q8HYP0 PRELIMINARY; PRT; 89 AA.
 AC Q8HYP0;
 DT 01-MAR-2003 (TEMBLrel. 23, Created)
 DT 01-MAR-2003 (TEMBLrel. 23, Last sequence update)
 DT 01-JUN-2003 (TEMBLrel. 24, Last annotation update)
 DE Chemokine CXCL12/SDP-1ALPHA.
 OS Macaca mulatta (Rhesus macaque).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecoidea; Macaca.
 OX NCBI_TaxID=9544;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22123042; PubMed=12126650;
 RA Basu S., Schaefer T.M., Ghosh M., Fuller C.L., Reinhardt T.A.,
 RT "Molecular cloning and sequencing of 25 different rhesus macaque
 RT chemokine cDNAs reveals evolutionary conservation among C, CC, CXC,
 RT AND CX3C families of chemokines."
 RL Cytokine 18:140-148(2002).
 RL Cytokine 18:140-148(2002).
 DR HSSP; P48061; ISDF.
 DR GO; GO:0005576; C:extracellular; IEA.
 DR GO; GO:0008009; F:chemokine activity; IEA.
 DR GO; GO:0006955; P:immune response; IEA.
 DR InterPro; IPR002473; C-X-C/Interlkn_8.
 DR InterPro; IPR001811; Chemokine_IL8.
 DR Pfam; PF00048; IL8; 1.
 DR PRINTS; PR00436; INTERLEUKIN8.
 DR SMART; SM00199; SCY; 1.
 SQ SEQUENCE 89 AA; 10105 MW; AD531633C6DC2B07 CRC64;
 Query Match 66.9%; Score 117; DB 2; Length 89;


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RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Parthenogenote;
RA Adachi U., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hirooka T., Hirozane T.,
RA Hori F., Imocant K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Kato H., Kawai J., Kojima Y., Kondo S., Kono H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ono M., Ohata N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.,
RA Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK045092; BAC32216.1; -.
SQ SEQUENCE 89 AA; 10032 MW; CAB8AD69078E55FA CRC64;

Query Match 66.9%; Score 117; DB 2; Length 89;
Best Local Similarity 40.3%; Pred. No. 6e-09;
Matches 27; Conservative 0; Mismatches 4; Indels 36; Gaps 1;

QY 1 KPVSLSYRCPCRFEGG-----GGLKXIQE 24
DB 22 KPVSLSYRCPCRFESHARANYKHLKILTPNCALQIVARLKNNNRQVCIDPKLXIQE 81
QY 25 YLEKALN 31
DB 82 YLEKALN 88

RESULT 6
BAC35845 PRELIMINARY; PRT; 89 AA.
AC BAC35845;
DT 14-APR-2004 (TREMBLrel. 27, Created)
DT 14-APR-2004 (TREMBLrel. 27, Last sequence update)
DE Adult male kidney cDNA, RIKEN full-length enriched library,
DE clone:0610039H13 product:retromal cell derived factor 1, full insert
DE sequence.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Kidney;
RX MEDLINE=22354683; PubMed=12466851;
RA The PANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs."
RL Nature 420:563-573 (2002).
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Kidney;
RX MEDLINE=21085660; PubMed=11217851;
RA RIKEN PANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection."
RL Nature 409:685-690 (2001).
[3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Kidney;
RX MEDLINE=99279253; PubMed=10349636;
RA Carninci P., Hayashizaki Y.,
RT "High-efficiency full-length cDNA cloning."
RL Mech. Enzymol. 303:19-44 (1999).
[4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Kidney;
RX MEDLINE=20499374; PubMed=11042159;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,

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RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.,
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes."
RL Genome Res. 10:1671-1630 (2000).
[5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Kidney;
RX MEDLINE=20530913; PubMed=11076861;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Kono H., Akiyama U., Nishi K., Kitesuna T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsunoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujimoto S., Inoue K., Togawa Y., Izawa M., Ohara E., Wataniki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsumura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer."
RL Genome Res. 10:1757-1771 (2000).
[6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Kidney;
RA Adachi U., Aizawa K., Akimura T., Aono H., Arai A.,
RA Arakawa T., Bono H., Hayatsu N., Hiramoto K., Hirooka T., Hori F.,
RA Hanagaki T., Hara A., Hayatsu N., Izawa M., Kasukawa T., Kato H.,
RA Imocant K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA Kawai J., Kojima Y., Kono H., Kouda M., Koya S., Kurihara C.,
RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ono M.,
RA Okazaki Y., Okido T., Owa C., Saito R., Saito R., Sakai C., Sakai K.,
RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA Teijima Y., Toya T., Yamamuro T., Yamana K., Yasunishi A.,
RA Yoshida K., Yoshino M., Muramatsu M., Hayashizaki Y.,
RA Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK075596; BAC35845.1; -.
SQ SEQUENCE 89 AA; 10032 MW; CAB8AD69078E55FA CRC64;

Query Match 66.9%; Score 117; DB 2; Length 89;
Best Local Similarity 40.3%; Pred. No. 6e-09;
Matches 27; Conservative 0; Mismatches 4; Indels 36; Gaps 1;

QY 1 KPVSLSYRCPCRFEGG-----GGLKXIQE 24
DB 22 KPVSLSYRCPCRFESHARANYKHLKILTPNCALQIVARLKNNNRQVCIDPKLXIQE 81
QY 25 YLEKALN 31
DB 82 YLEKALN 88

RESULT 7
CAG32979 PRELIMINARY; PRT; 89 AA.
AC CAG32979;
DT 20-MAY-2004 (TREMBLrel. 27, Created)
DT 20-MAY-2004 (TREMBLrel. 27, Last sequence update)
DE 20-MAY-2004 (TREMBLrel. 27, Last annotation update)
DE CXC12 protein (Fragment).
GN CXC12.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
[1]
RP SEQUENCE FROM N.A.
RA Ebert U., Schick M., Neubert P., Schattner R., Henze S., Korn B.,
RT "Cloning of human full open reading frames in Gateway (TM) system entry
RT vector (pDONR201)."
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CR450283; CAG32979.1; -.
FT NON TER 89
SQ SEQUENCE 89 AA; 10103 MW; 62B44B8D209C3A14 CRC64;

Query Match 66.9%; Score 117; DB 2; Length 89;

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Best Local Similarity 40.3%; Pred. No. 6e-09;
Matches 27; Conservative 0; Mismatches 4; Indels 36; Gaps 1;

QY 1 KPVSLSYRCPCRFPGG-----GGKMKIOE 24
DB 22 KPVSLSYRCPCRFESHVAVANVHKLITNPNCALQIVARLKNRRVOCIDPKLKWIOE 81

QY 25 YLEKALN 31
DB 82 YLEKALN 88

RESULT 8

Q9H554 PRELIMINARY; PRT; 92 AA.

AC Q9H554;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE BA20J15.1.2 (Stromal cell-derived factor 1, isoform beta)
DE (Fragment).
GN Name=SDP1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Blvd C.;
RL Submitted (SEP-2000) to the EMBL/Genbank/DBJ databases.
DR EMBL; AL137026; CAC10202.1; -
DR HSSP; P48061; ISDF.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0008009; F:chemokine activity; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR002473; C-X-C/Interlkn_8.
DR InterPro; IPR001811; Chemokine_IL8.
DR Pfam; PF00048; IL8; 1.
DR PRINTS; PR00436; INTERLEUKIN8.
DR SMART; SM00199; SCY; 1.
FT NON TER
SQ SEQUENCE 92 AA; 10510 MW; AEF0CA02B448BD20 CRC64;

Query Match 66.9%; Score 117; DB 2; Length 92;
Best Local Similarity 40.3%; Pred. No. 6.2e-09;
Matches 27; Conservative 0; Mismatches 4; Indels 36; Gaps 1;

QY 1 KPVSLSYRCPCRFPGG-----GGKMKIOE 24
DB 22 KPVSLSYRCPCRFESHVAVANVHKLITNPNCALQIVARLKNRRVOCIDPKLKWIOE 81

QY 25 YLEKALN 31
DB 82 YLEKALN 88

RESULT 9

SDP1_FELCA STANDARD; PRT; 93 AA.

AC Q62657;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 05-JUN-2004 (Rel. 44, Last annotation update)
DE Stromal cell-derived factor 1 precursor (SDF-1) (CXCL12).
GN Name=CXCL12; Synonyms=SDP1;
OS Feline silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Placentalia; Felidae; Felis.
OX NCBI_Taxid=9685;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS ALPHA AND BETA).
RC TISSUE=Thymus;
MEDLINE=98450506; PubMed=9777331;

RA Nishimura Y., Miyazawa T., Ikeda Y., Izumiya Y., Nakamura K.,
RA Cai J.S., Sato E., Kohmoto M., Mikami T.;
RT "Molecular cloning and sequencing of feline stromal cell-derived
RT factor-1 alpha and beta."
RL Eur. J. Immunogenet. 25:303-305(1998).
CC -1- FUNCTION: Chemottractant active on T-lymphocytes, monocytes, but
CC not neutrophils.
CC -1- SUBCELLULAR LOCATION: Secreted.

CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=Beta;
CC Name=Alpha;
CC IsoId=O62657-1; Sequence=Displayed;
CC IsoId=O62657-2; Sequence=VSP_001055;
CC -1- SIMILARITY: Belongs to the intercrine alpha (chemokine Cxc)
CC family.

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CC or send an email to license@isb-sib.ch).

CC EMBL; AB011966; BA28602.1; -
DR HSSP; P48061; ISDF.
DR InterPro; IPR002473; C-X-C/Interlkn_8.
DR InterPro; IPR001811; Chemokine_IL8.
DR InterPro; IPR001089; CXC_chemokine_small.
DR Pfam; PF00048; IL8; 1.
DR PRINTS; PR00436; INTERLEUKIN8.
DR SMART; SM00199; SCY; 1.
DR PROSITE; PS00471; SMALL_CYTOKINES_CXC; FALSE NEG.
KW Alternative splicing; Chemotaxis; Cytokine; Growth factor; Signal.
FT SIGNAL 1 21
FT CHAIN 22 93
FT DISULFID 30 55
FT DISULFID 32 71
FT VARSPLIC 90 93
FT FTId=VSP_001055.
SQ SEQUENCE 93 AA; 10581 MW; 44FC763711B9BE37 CRC64;

Query Match 66.9%; Score 117; DB 1; Length 93;
Best Local Similarity 40.3%; Pred. No. 6.3e-09;
Matches 27; Conservative 0; Mismatches 4; Indels 36; Gaps 1;

QY 1 KPVSLSYRCPCRFPGG-----GGKMKIOE 24
DB 22 KPVSLSYRCPCRFESHVAVANVHKLITNPNCALQIVARLKNRRVOCIDPKLKWIOE 81

QY 25 YLEKALN 31
DB 82 YLEKALN 88

RESULT 10

SDP1_HUMAN STANDARD; PRT; 93 AA.

AC P48061;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE Stromal cell-derived factor 1 precursor (SDF-1) (CXCL12) (pre-B cell
DE growth stimulating factor) (PBSF) (HIRH) (Contains: SDF-1-beta(3-72);
DE SDF-1-alpha(3-67)).
GN Name=CXCL12; Synonyms=SDP1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.

RA Spocchia L.D.;
 RL Submitted (OCT-1994) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=9603262; PubMed=7490086;
 RA Shirozu M., Nakano T., Inazawa J., Tashiro K., Tada H., Shinohara T.,
 RT Honjo T.;
 RL "Structure and chromosomal localization of the human stromal cell-
 RT derived factor 1 (SDF1) gene.";
 RL Genomics 28:495-500(1995).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM ALPHA).
 RC TISSUE=Liver;
 RA Begum N.A., Barnard G.F.;
 RT "Nucleotide sequence of hIRH, human interleukin reduced in hepatomas.";
 RL Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RX PubMed=15164054; DOI=10.1038/nature02462;
 RA Deloukas P., Barthrowl M.E., Grahame D.V., Rubinfeld M., French L.,
 RA Steward C.A., Sims S.K., Jones M.C., Searle S., Scott C., Howe K.,
 RA Hunt S.E., Andrews T.D., Gilbert J.G.R., Svardbeck D., Ashurst J.L.,
 RA Taylor A., Batties J., Bird C.P., Alencough R., Almeida J.P.,
 RA Ashwell R.I.S., Ambrose K.D., Babbage A.K., Bagguley C.D., Bailey J.,
 RA Banerjee R., Bates K., Beasley H., Bray-Allen S., Brown A.J.,
 RA Brown J.V., Burford D.C., Burrill W., Burton J., Cahill P., Cantre D.,
 RA Carter N.P., Chapman J.C., Clark S.V., Clarke G., Clee C.M., Clegg S.,
 RA Corby N., Coulson A., Dhali P., Dutta I., Dunn M., Faulkner L.,
 RA Frankish A., Frankland J.A., Garner P., Garnett J., Griddle S.,
 RA Griffiths C., Grocock R., Gustafson E., Hammond S., Harley J.,
 RA Hart E., Heath P.D., Ho T.P., Hopkins B., Horne J., Howden P.J.,
 RA Hickle E., Hynds C., Johnson C., Johnson D., Kana A., Kay M.,
 RA Kimberley A.M., Kershaw J.K., Kokkinaki M., Laird G., Lawlor S.,
 RA Lee H.M., Leongamornlert D.A., Laird G., Lloyd C., Lloyd D.M.,
 RA Loveland J., Lovell J., McLaren S., McLeay K.E., McMurtry A.,
 RA Mashrafi-Mohammadi M., Matthews L., Milne S., Nickerson T.,
 RA Nguyen M., Overton-Larty E., Palmer S.A., Pearce A.V., Peck A.I.,
 RA Peltan S., Phillimore B., Porter K., Rice C.M., Rogosin A., Ross M.T.,
 RA Sarrafidou T., Shira H.K., Showkhen R., Skuce C.D., Smith M.,
 RA Standing L., Sycamore N., Tester J., Thorpe A., Torcaso W.,
 RA Tracey A., Tromans A., Tsoias J., Wall M., Walsh J., Wang H.,
 RA Weinsteck K., West A.P., Willey D.L., Whithead S.L., Wilming L.,
 RA Way P.W., Young L., Chen Y., Lovering R.C., Moschonas N.K.,
 RA Webster R., Fichtel K., Bentley D., Durbin R., Hubbard T.,
 RA Doucette-Stamm L., Beck S., Smith D.R., Rogers J.;
 RL "The DNA sequence and comparative analysis of human chromosome 10.";
 RL Nature 429:375-381(2004).
 RN [5]
 RP SEQUENCE FROM N.A. (ISOFORM ALPHA).
 RC TISSUE=Brain;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strauberg R.L., Felting B.A., Grouse L.H., Derge U.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shemmen C.W., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Scapellato M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Uedin T.B., Tothlyuk S., Carninci P., Prange C.,
 RA Rana S.S., Loguallano N.A., Peters G.J., Adamson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Gilmwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallie D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16699-16903(2002).
 RN [6]
 RP IDENTIFICATION OF SDF-1ALPHA(3-67) AND SDF-1BETA(3-72) BY MASS

RP SPECTROMETRY, AND N-TERMINAL AND C-TERMINAL PROCESSING.
 RX PubMed=14525775; DOI=10.1182/blood-2003-08-2857;
 RA De la Luz Sierra M., Yang F., Marazaki M., Salvucci O., Davis D.,
 RA Yarchan R., Zhang H.H., Fales H., Toato G.;
 RT "Differential processing of stromal-derived factor-1alpha and beta
 RT explains functional diversity.";
 RL Blood 103:2452-2459(2004).
 RN [7]
 RP STRUCTURE BY NMR OF 22-88.
 RX MEDLINE=96046030; PubMed=9384579;
 RA Crump M.P., Gong J.H., Loetscher P., Rajaratnam K., Amara A.,
 RA Azenzana-Seladedos F., Vitellizier J.L., Baggiolini M., Sykes B.D.,
 RA Clark-Lewis I.;
 RT "Solution structure and basis for functional activity of stromal cell-
 RT derived factor-1; dissociation of CXCR4 activation from binding and
 RT inhibition of HIV-1.";
 RL EMO J. 16:6996-7007(1997).
 RN [8]
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 22-88.
 RX MEDLINE=98284037; PubMed=9618518;
 RA Dealwis C., Fernandez E.J., Thompson D.A., Simon R.J., Stani M.A.,
 RA Lolit E.;
 RT "Crystal structure of chemically synthesized (N3A) stromal cell-
 RT derived factor 1alpha, a potent ligand for the HIV-1 'Fusin'
 RT coreceptor.";
 RL Proc. Natl. Acad. Sci. U.S.A. 95:6941-6946(1998).
 CC -1- FUNCTION: Chemotactant active on T-lymphocytes, monocytes, but
 CC not neutrophils. SDF-1-beta(3-72) and SDF-1-alpha(3-67) show a
 CC reduced chemotactic activity. Binding to cell surface
 CC proteoglycans seems to inhibit formation of SDF-1-alpha(3-67) and
 CC thus to preserve activity on local sites.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=Beta; Synonyms=SDF-1-beta(1-72);
 CC IsoId=P48061-1; Sequence=Displayed;
 CC Name=Alpha; Synonyms=SDF-1-alpha(1-68);
 CC IsoId=P48061-2; Sequence=VSP 001056;
 CC -1- PTM: Processed forms SDF-1-beta(3-72) and SDF-1-alpha(3-67) are
 CC produced after secretion by proteolytic cleavage of isoforms Beta
 CC and Alpha, respectively. The N-terminal processing is probably
 CC achieved by DPP4. Isoform Alpha is first cleaved at the C-terminus
 CC to yield a SDF-1-alpha(1-67) intermediate before being processed
 CC at the N-terminus. The C-terminal processing of isoform Alpha is
 CC reduced by binding to heparin and, probably, cell surface
 CC proteoglycans.
 CC -1- SIMILARITY: Belongs to the Interleukin alpha (chemokine CXC)
 CC family.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: U16752; AAA97434.1; -
 DR EMBL: L36033; AAB39332.1; -
 DR EMBL: L36034; AAB39333.1; -
 DR EMBL: U19495; AAB40516.1; -
 DR EMBL: AL337026; CAC10203.1; -
 DR EMBL: BC039893; AAB39893.1; -
 DR EMBL: G01540; G01540.
 DR PDB: 1A15; X-ray; A/B=22-88.
 DR PDB: 1Q67; X-ray; A/B=22-88.
 DR PDB: 1SDF; NMR; @=22-88.
 DR PDB: 2SDF; NMR; @=22-88.
 DR GeneW: HGNC:10672; CXCL12.
 DR MIM: 600835; -
 DR GO: GO:0008009; P:chemokine activity; TAS.
 DR GO: GO:0005102; P:receptor binding; TAS.
 DR GO: GO:0006874; P:calcium ion homeostasis; TAS.

```
DR GO:0007155; P:cell adhesion; TAS.
DR GO:0006935; P:chemotaxis; TAS.
DR GO:0008015; P:circulation; TAS.
DR GO:0007165; P:G-protein coupled receptor protein signalin. . .; TAS.
DR GO:0006955; P:immune response; TAS.
DR GO:0008065; P:regulation of actin polymerization and/or d. . .; TAS.
DR GO:0009615; P:response to virus; TAS.
DR GO:0007165; P:signal transduction; TAS.
DR InterPro: IPR02473; C-X-C/Interlkn_8.
DR InterPro: IPR001811; Chemokine_IL8.
DR InterPro: IPR001089; CXC_chemokine_small.
DR Pfam: PF00048; IL8; 1.
DR PRINTS: PR00436; INTERLEUKIN8.
DR PROSITE: PS00471; SMALL_CYTOKINES_CXC; FALSE_NEG.
DR 3D-structure; Alternative splicing; Chemotaxis; Cytokine;
DR Growth factor; Signal.
FT SIGNAL 1 21 Potential.
FT CHAIN 22 93 Stromal cell-derived factor 1.
FT CHAIN 24 93 SDF-1beta(3-72).
FT CHAIN 24 88 SDF-1alpha(3-67).
FT DISULFID 30 55
FT DISULFID 32 71
FT VASAPLIC 90 93 Missing (in isoform Alpha).
FT STRAND 36 36 /FtId=VSP_001056.
FT HELIX 41 43
FT STRAND 44 50
FT TURN 53 54
FT STRAND 59 63
FT TURN 64 66
FT STRAND 69 72
FT TURN 74 75
FT HELIX 77 82
FT TURN 83 83
FT HELIX 84 87
SQ SEQUENCE 93 AA; 10666 MW; 505B5A29C2B44E8D CRC64;

Query Match 66.9%; Score 117; DB 1; Length 93;
Best Local Similarity 40.3%; Pred. No. 6.3e-09;
Matches 27; Conservative 0; Mismatches 4; Indels 36; Gaps 1;

QY 1 KPVSLSRCPGRFEGG-----GGKMKIQE 24
   |||||
Db 22 KPVSLSRCPGRFEGSHVAVANVHKLINTPNCALQIVARLKNRNQVCIDPKLKIQE 81
   |||||
QY 25 YLEKALN 31
   |||||
Db 82 YLEKALN 88

RESULT 11
Q6EKW4 PRELIMINARY; PRT; 116 AA.
AC Q6EKW4;
DT 01-OCT-2004 (TREMblrel. 28, Created)
DT 01-OCT-2004 (TREMblrel. 28, Last sequence update)
DT 01-OCT-2004 (TREMblrel. 28, Last annotation update)
DE CxCL12 chemokine.
GN Name=CxCL12;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxId=9623;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed15242943;
RA Ledger T.N., Pinton P., Bourges D., Rouni P., Salmon H., Oswald I.P.;
RT "Development of a macroarray to specifically analyze immunological
   gene expression in swine."
RL Clin. Diagn. Lab. Immunol. 11:691-698 (2004).
DR EMBL; AY312066; AA084094.1; -.
SQ SEQUENCE 116 AA; 12622 MW; 2A1BCR0551C2BEAB CRC64;
```

```
Query Match 66.9%; Score 117; DB 2; Length 116;
Best Local Similarity 40.3%; Pred. No. 7.8e-09;
Matches 27; Conservative 0; Mismatches 4; Indels 36; Gaps 1;

QY 1 KPVSLSRCPGRFEGG-----GGKMKIQE 24
   |||||
Db 22 KPVSLSRCPGRFEGSHVAVANVHKLINTPNCALQIVARLKNRNQVCIDPKLKIQE 81
   |||||
QY 25 YLEKALN 31
   |||||
Db 82 YLEKALN 88

RESULT 12
Q80ZM4 PRELIMINARY; PRT; 137 AA.
AC Q80ZM4;
DT 01-JUN-2003 (TREMblrel. 24, Created)
DT 01-JUN-2003 (TREMblrel. 24, Last sequence update)
DT 01-MAR-2004 (TREMblrel. 26, Last annotation update)
DE Cxcl12 protein.
GN Name=Cxcl12;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6; TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Alecnul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toobyuki S., Carninci P., Prange C.,
RA Rata S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mulhaly S.J.,
RA Bosak S.A., McEwan P.U., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Wozley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Vallier J., Helton E., Kettman M., Madan A., Young A.C., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W., Butlerfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallie D.E., Schnerch A., Schein J.B.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
   and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6; TISSUE=Brain;
RA Strausberg R.;
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC046827; AA046827.1; -.
DR HSSP; P48061; 1SDF.
DR MGD; MGI:103556; Cxcl12.
DR GO:0008009; P:chemokine activity; IDA.
DR GO:0007420; P:brain development; IDA.
DR GO:0007281; P:brain cell development; IDA.
DR GO:0008354; P:germ cell migration; IDA.
DR GO:0050930; P:induction of positive chemotaxis; IDA.
DR GO:0030335; P:positive regulation of cell migration; IDA.
DR GO:0042098; P:T-cell proliferation; IMP.
DR InterPro: IPR02473; C-X-C/Interlkn_8.
DR InterPro: IPR001811; Chemokine_IL8.
DR Pfam; PF00048; IL8; 1.
DR PRINTS; PR00436; INTERLEUKIN8.
DR SMART; SM00199; SCY; 1.
SQ SEQUENCE 137 AA; 15529 MW; 04B47DAB6904DF77 CRC64;

Query Match 66.9%; Score 117; DB 2; Length 137;
```


GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 4, 2005, 15:43:59 ; Search time 61.9672 Seconds
(without alignments)
173.671 Million cell updates/sec

Title: US-10-086-177a-12

Perfect score: 169
Sequence: 1 KPVSLSYRCRCRFGGGLKWIQVLEKALN 30

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database: A_Geneseq_23Sep04:*

1: geneseqp1980s:*\n2: geneseqp1990s:*\n3: geneseqp2000s:*\n4: geneseqp2001s:*\n5: geneseqp2002s:*\n6: geneseqp2003as:*\n7: geneseqp2003bs:*\n8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	169	100.0	30	5 AAB47694	Aab47694 SDF-1(1-1)
2	169	100.0	30	5 AAB47692	Aab47692 SDF-1(1-1)
3	158.5	93.8	31	3 AAB28545	Aab28545 Chemokine
4	158.5	93.8	31	5 AAB47693	Aab47693 SDF-1(1-1)
5	158.5	93.8	31	5 AAB47686	Aab47686 SDF-1(1-1)
6	158.5	93.8	31	5 AAB47706	Aab47706 SDF-1(1-1)
7	158.5	93.8	31	5 AAB47702	Aab47702 SDF-1(1-1)
8	158.5	93.8	31	5 AAB47717	Aab47717 SDF-1(1-1)
9	158.5	93.8	31	5 AAB47715	Aab47715 SDF-1(1-1)
10	158.5	93.8	31	5 AAB47716	Aab47716 SDF-1(1-1)
11	158.5	93.8	31	5 AAB47695	Aab47695 SDF-1(1-1)
12	158.5	93.8	31	5 AAB47700	Aab47700 SDF-1(1-1)
13	158.5	93.8	31	5 AAB47703	Aab47703 SDF-1(1-1)
14	158.5	93.8	31	5 AAB47714	Aab47714 SDF-1(1-1)
15	158.5	93.8	31	5 AAB47701	Aab47701 SDF-1(1-1)
16	158.5	93.2	33	5 AAB47698	Aab47698 SDF-1(1-1)
17	157.5	93.2	33	5 AAB47696	Aab47696 SDF-1(1-1)
18	157.5	92.9	34	5 AAB47697	Aab47697 SDF-1(1-1)
19	157	92.9	34	5 AAB47699	Aab47699 SDF-1(1-1)
20	155.5	92.0	31	5 AAB47705	Aab47705 SDF-1(1-1)
21	155.5	92.0	31	5 AAB47704	Aab47704 SDF-1(1-1)
22	149.5	88.5	31	5 AAM48698	Aam48698 CXCR4 cyc
23	148	87.6	34	5 AAM48699	Aam48699 CXCR4 cyc
24	138.5	82.0	27	3 AAB28544	Aab28544 Chemokine

26	132.5	78.4	25	3 AAB28546	Aab28546 Chemokine
27	130	76.9	28	5 AAM48673	Aam48673 CXCR4 pep
28	128.5	76.0	31	5 AAM48674	Aam48674 CXCR4 pep
29	125	74.0	28	5 AAM48676	Aam48676 CXCR4 pep
30	123.5	73.1	31	5 AAM48680	Aam48680 CXCR4 pep
31	123	72.8	28	5 AAM48678	Aam48678 CXCR4 pep
32	123	72.8	28	5 AAM48675	Aam48675 CXCR4 pep
33	121.5	71.9	31	5 AAM48682	Aam48682 CXCR4 pep
34	121.5	71.9	31	5 AAM48681	Aam48681 CXCR4 pep
35	120	71.0	28	5 AAM48677	Aam48677 CXCR4 pep
36	118.5	70.1	31	5 AAM50760	Aam50760 Peptide w
37	118.5	70.1	67	2 AAY06726	Aay06726 Amino aci
38	118.5	70.1	67	2 AAY06741	Aay06741 SDF-1 alp
39	118.5	70.1	67	2 AAY34092	Aay34092 Native sc
40	118.5	70.1	67	2 AAY67594	Aay67594 SDF-1 alp
41	118.5	70.1	67	3 AAB47680	Aab47680 SDF-1 alp
42	118.5	70.1	67	5 AAB47689	Aab47689 SDF-1 alp
43	118.5	70.1	67	5 AAB47689	Aab47689 SDF-1 alp
44	118.5	70.1	67	7 ADF79402	Adf79402 Chemokine

ALIGNMENTS

RESULT 1	
AAB47694	AAB47694 standard; peptide; 30 AA.
ID	AAB47694; (first entry)
AC	30-JAN-2002
DT	SDF-1(1-14) - (G)3 - SDF-1(55-67) amide.
DE	Hematopoietic cell; multiplications; CXCR4 chemokine receptor 4; CXCR4; agonist; stromal cell derived factor one; SDF-1; autoimmune disease; macrophage inflammatory protein 1-alpha; MIP-1-alpha; cancer; autologous; allogenic; bone marrow; stem cell; transplantation.
KM	Synthetic.
OS	
XX	
FT	Key Location/Qualifiers
FT	Modified-site 30 /note="C-terminal amide"
FT	
PN	WO200176615-A2.
XX	
PD	18-OCT-2001.
XX	
PF	12-APR-2001; 2001WO-CA000540.
XX	
PR	12-APR-2000; 2000CA-02305036.
PR	14-SEP-2000; 2000US-0232425P.
PR	23-FEB-2001; 2001CA-02335109.
XX	
PA	(UYBR-) UNIV BRITISH COLUMBIA.
PA	(CHEM-) CHEMOKINE THERAPEUTICS CORP.
PI	Salari H, Mezrouk A, Arab L, Tudan CR, Saxena G, Eaves CJ, Cashman J, Clark-Lewis I,
PI	WPI; 2002-025882/03.
XX	
DR	
XX	
PT	CXCR4 receptor 4 agonists that reduces hematopoietic cell multiplication and susceptibility to cytotoxic agents, are useful for bone marrow or peripheral blood stem cell transplantation.
PT	
XX	
PS	Example 1; Page 42; 74pp; English.
XX	
CC	The sequences given in AAB47680-717 represent peptides which may be used in the method of the invention for reducing the rate of hematopoietic cell multiplication. These peptides act as CXCR4 chemokine receptor 4

CC (CXCR4) agonists to the cells. These peptides are based on stromal cell
 CC derived factor one (SDF-1) with some also containing sequences derived
 CC from macrophage inflammatory protein 1-alpha (MIP-1-alpha). They can be
 CC used to reduce susceptibility of hematopoietic cells to a cytotoxic
 CC agent, by administering one of the agonist peptides to the cells prior to
 CC or during exposure of the cells to the cytotoxic agent. The CXCR4 agonist
 CC is used to reduce susceptibility of hematopoietic cells to a cytotoxic
 CC agent, particularly in a patient with cancer requiring autologous or
 CC allogeneic bone marrow or peripheral blood stem cell transplantation, or
 CC an autoimmune disease

XX SQ Sequence 30 AA;

Query Match 100.0%; Score 169; DB 5; Length 30;
 Best Local Similarity 100.0%; Pred. No. 1.5e-16;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPVSLSYRCPCRFPGGGLKMWIOEYLEKALN 30
 Db 1 KPVSLSYRCPCRFPGGGLKMWIOEYLEKALN 30

RESULT 2
 AAB47692 standard; peptide; 30 AA.

XX AAB47692;
 AC
 XX
 DT 30-JAN-2002 (first entry)
 XX
 DE SDF-1(1-14) - (G)3 - SDF-1(55-67) acid.
 XX
 KM Haematopoietic cell; multiplication; CXCR chemokine receptor 4; CXCR4;
 KM agonist; stromal cell derived factor one; SDF-1; autoimmune disease;
 KM macrophage inflammatory protein 1-alpha; MIP-1-alpha; cancer; autologous;
 KM allogenic; bone marrow; stem cell; transplantation.
 XX
 OS Synthetic.
 XX
 PN WO200176615-A2.
 PD 18-OCT-2001.
 XX
 PF 12-APR-2001; 2001WO-CA000540.
 XX
 PR 12-APR-2000; 2000CA-02305036.
 PR 14-SEP-2000; 2000US-0232425P.
 PR 23-FEB-2001; 2001CA-02335109.
 XX
 PA (UYBR-) UNIV BRITISH COLUMBIA.
 PA (CHEM-) CHEMOKINE THERAPEUTICS CORP.
 XX
 PI Salari H, Merzouk A, Arab L, Tudan CR, Saxena G, Eaves CJ;
 PI Cashman J, Clark-Lewis I;
 PI
 DR WPI; 2002-025882/03.
 XX
 PT CXCR receptor 4 agonists that reduces hematopoietic cell multiplication
 PT and susceptibility to cytotoxic agents, are useful for bone marrow or
 PT peripheral blood stem cell transplantation.
 XX
 PS Example 1; Page 42; 74pp; English.
 XX
 CC The sequences given in AAB47680-717 represent peptides which may be used
 CC in the method of the invention for reducing the rate of hematopoietic
 CC cell multiplication. These peptides act as CXCR chemokine receptor 4
 CC (CXCR4) agonists to the cells. These peptides are based on stromal cell
 CC derived factor one (SDF-1) with some also containing sequences derived
 CC from macrophage inflammatory protein 1-alpha (MIP-1-alpha). They can be
 CC used to reduce susceptibility of hematopoietic cells to a cytotoxic
 CC agent, by administering one of the agonist peptides to the cells prior to
 CC or during exposure of the cells to the cytotoxic agent. The CXCR4 agonist
 CC is used to reduce susceptibility of hematopoietic cells to a cytotoxic

CC agent, particularly in a patient with cancer requiring autologous or
 CC allogeneic bone marrow or peripheral blood stem cell transplantation, or
 CC an autoimmune disease

XX SQ Sequence 30 AA;

Query Match 100.0%; Score 169; DB 5; Length 30;
 Best Local Similarity 100.0%; Pred. No. 1.5e-16;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPVSLSYRCPCRFPGGGLKMWIOEYLEKALN 30
 Db 1 KPVSLSYRCPCRFPGGGLKMWIOEYLEKALN 30

RESULT 3
 AAB28545 standard; peptide; 31 AA.

XX AAB28545;
 AC
 XX
 DT 08-FEB-2001 (first entry)
 XX
 DE Chemokine-derived synthetic peptide #5.
 XX
 KM Chemokine-derived synthetic peptide; anti-HIV;
 KM stromal cell-derived factor-1; SDF-1; Human immunodeficiency virus-1;
 KM HIV-1; CXCR chemokine receptor 4; CXCR4.
 XX
 OS Synthetic.
 XX
 PN WO200059928-A1.
 PD 12-OCT-2000.
 XX
 PF 06-APR-2000; 2000WO-US009236.
 XX
 PR 07-APR-1999; 99US-0128106P.
 XX
 PA (UYJE-) UNIV JEFFERSON THOMAS.
 PA
 PI Huang Z, Luo Z, Zhou N, Luo J;
 PI
 DR WPI; 2000-686931/67.
 XX
 PT Novel synthetic chemokine peptides of stromal cell derived factor useful
 PT for inhibiting HIV-1 entry and infection via CXCR chemokine receptor-4,
 PT and in HIV infection treatment and prophylaxis.
 XX
 PS Claim 14; Page 43; 56pp; English.
 XX
 CC The present sequence is a synthetic chemokine peptide of the chemokine
 CC stromal cell-derived factor-1 (SDF-1). It is useful for inhibiting the
 CC entry of Human immunodeficiency virus-1 (HIV-1) into CXCR chemokine
 CC receptor 4 (CXCR4)-expressing cells and for treating HIV infection. The
 CC novel SDF-1 derived synthetic peptides have enhanced activity over
 CC separate peptides derived only from the N-terminal segment of SDF-1 or
 CC derived only from the C-terminal region of SDF-1

XX SQ Sequence 31 AA;

Query Match 93.8%; Score 158.5; DB 3; Length 31;
 Best Local Similarity 96.8%; Pred. No. 4.8e-15;
 Matches 30; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 KPVSLSYRCPCRFPGGGLKMWIOEYLEKALN 30
 Db 1 KPVSLSYRCPCRFPGGGLKMWIOEYLEKALN 31

RESULT 4
 AAB47693 standard; peptide; 31 AA.

XX AAB47693;
 AC 30-JAN-2002 (first entry)
 DT SDF-1(1-14) - (G)4 - SDF-1(55-67) acid.
 DE
 XX
 KW Hematopoietic cell; multiplication; CXK chemokine receptor 4; CXCR4;
 KW agonist; stromal cell derived factor one; SDF-1; autoimmune disease;
 KW macrophage inflammatory protein 1-alpha; MIP-1-alpha; cancer; autologous;
 KW allogenic; bone marrow; stem cell; transplantation.
 XX
 OS Synthetic.
 XX
 PN WO200176615-A2.
 XX 18-OCT-2001.
 PD
 XX 12-APR-2001; 2001WO-CA000540.
 PF
 XX 12-APR-2000; 2000CA-02305036.
 PR 14-SEP-2000; 2000US-0232425P.
 PR 23-FEB-2001; 2001CA-02335109.
 XX
 PA (UYBR-) UNIV BRITISH COLUMBIA.
 PA (CHEM-) CHEMOKINE THERAPEUTICS CORP.
 PI Salari H, Merzouk A, Arab L, Tudan CR, Saxena G, Eaves CJ,
 PI Cashman J, Clark-Lewis I;
 PI
 XX
 DR WPI; 2002-025882/03.
 XX
 PT CXK receptor 4 agonists that reduces hematopoietic cell multiplication
 PT and susceptibility to cytotoxic agents, are useful for bone marrow or
 PT peripheral blood stem cell transplantation.
 PS
 XX Example 1; Page 42; 74pp; English.
 CC The sequences given in AAB47680-717 represent peptides which may be used
 CC in the method of the invention for reducing the rate of hematopoietic
 CC cell multiplication. These peptides act as CXK chemokine receptor 4
 CC (CXCR4) agonists to the cells. These peptides are based on stromal cell
 CC derived factor one (SDF-1) with some also containing sequences derived
 CC from macrophage inflammatory protein 1-alpha (MIP-1-alpha). They can be
 CC used to reduce susceptibility of hematopoietic cells to a cytotoxic
 CC agent, by administering one of the agonist peptides to the cells prior to
 CC or during exposure of the cells to the cytotoxic agent. The CXCR4 agonist
 CC is used to reduce susceptibility of hematopoietic cells to a cytotoxic
 CC agent, particularly in a patient with cancer requiring autologous or
 CC allogenic bone marrow or peripheral blood stem cell transplantation, or
 CC an autoimmune disease
 XX
 SQ Sequence 31 AA;
 XX
 Query Match 93.8%; Score 158.5; DB 5; Length 31;
 Best Local Similarity 96.8%; Pred. No. 4.8e-15;
 Matches 30; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
 QY 1 KPVSLSYRCPCRFPGGGLKMWIOEYLEKALN 30
 DB 1 KPVSLSYRCPCRFPGGGLKMWIOEYLEKALN 31
 XX
 RESULT 5
 AAB47686
 ID AAB47686 standard; peptide; 31 AA.
 XX
 AC AAB47686;
 XX
 DT 30-JAN-2002 (first entry)
 XX
 DE SDF-1(1-14) - (G)4 - SDF-1(56-67).
 XX

KW Hematopoietic cell; multiplication; CXK chemokine receptor 4; CXCR4;
 KW agonist; stromal cell derived factor one; SDF-1; autoimmune disease;
 KW macrophage inflammatory protein 1-alpha; MIP-1-alpha; cancer; autologous;
 KW allogenic; bone marrow; stem cell; transplantation.
 XX
 OS Synthetic.
 XX
 PN WO200176615-A2.
 XX 18-OCT-2001.
 PD
 XX 12-APR-2001; 2001WO-CA000540.
 PF
 XX 12-APR-2000; 2000CA-02305036.
 PR 14-SEP-2000; 2000US-0232425P.
 PR 23-FEB-2001; 2001CA-02335109.
 XX
 PA (UYBR-) UNIV BRITISH COLUMBIA.
 PA (CHEM-) CHEMOKINE THERAPEUTICS CORP.
 PI Salari H, Merzouk A, Arab L, Tudan CR, Saxena G, Eaves CJ,
 PI Cashman J, Clark-Lewis I;
 PI
 XX
 DR WPI; 2002-025882/03.
 XX
 PT CXK receptor 4 agonists that reduces hematopoietic cell multiplication
 PT and susceptibility to cytotoxic agents, are useful for bone marrow or
 PT peripheral blood stem cell transplantation.
 PS
 XX Claim 8; Page 58; 74pp; English.
 CC The sequences given in AAB47680-717 represent peptides which may be used
 CC in the method of the invention for reducing the rate of hematopoietic
 CC cell multiplication. These peptides act as CXK chemokine receptor 4
 CC (CXCR4) agonists to the cells. These peptides are based on stromal cell
 CC derived factor one (SDF-1) with some also containing sequences derived
 CC from macrophage inflammatory protein 1-alpha (MIP-1-alpha). They can be
 CC used to reduce susceptibility of hematopoietic cells to a cytotoxic
 CC agent, by administering one of the agonist peptides to the cells prior to
 CC or during exposure of the cells to the cytotoxic agent. The CXCR4 agonist
 CC is used to reduce susceptibility of hematopoietic cells to a cytotoxic
 CC agent, particularly in a patient with cancer requiring autologous or
 CC allogenic bone marrow or peripheral blood stem cell transplantation, or
 CC an autoimmune disease
 XX
 SQ Sequence 31 AA;
 XX
 Query Match 93.8%; Score 158.5; DB 5; Length 31;
 Best Local Similarity 96.8%; Pred. No. 4.8e-15;
 Matches 30; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
 QY 1 KPVSLSYRCPCRFPGGGLKMWIOEYLEKALN 30
 DB 1 KPVSLSYRCPCRFPGGGLKMWIOEYLEKALN 31
 XX
 RESULT 6
 AAB47706
 ID AAB47706 standard; peptide; 31 AA.
 XX
 AC AAB47706;
 XX
 DT 30-JAN-2002 (first entry)
 XX
 DE SDF-1(1-14) - (G)4 - SDF-1(55-67)-G9/C11-cyclic acid.
 XX
 KW Hematopoietic cell; multiplication; CXK chemokine receptor 4; CXCR4;
 KW agonist; stromal cell derived factor one; SDF-1; autoimmune disease;
 KW macrophage inflammatory protein 1-alpha; MIP-1-alpha; cancer; autologous;
 KW allogenic; bone marrow; stem cell; transplantation.
 XX
 OS Synthetic.
 XX

Key	Location/Qualifiers
Key	Location/Qualifiers
Disulfide-bond	9.11
WO200176615-A2.	
18-OCT-2001.	
12-APR-2001; 2001WO-CA000540.	
12-APR-2000; 2000CA-02305036.	
14-SEP-2000; 2000US-0232425P.	
23-FEB-2001; 2001CA-02335109.	
(UYBR-) UNIV BRITISH COLUMBIA.	
(CHEM-) CHEMOKINE THERAPEUTICS CORP.	
Salari H, Merzouk A, Arab L, Tudan CR, Saxena G, Eaves CJ, Cashman J, Clark-Lewis I,	
WPI; 2002-025882/03.	
Example 1; Page 44; 74pp; English.	
The sequences given in AAB47680-717 represent peptides which may be used in the method of the invention for reducing the rate of hematopoietic cell multiplication. These peptides act as CXCR4 chemokine receptor 4 (CXCR4) agonists to the cells. These peptides are based on stromal cell derived factor one (SDF-1) with some also containing sequences derived from macrophage inflammatory protein 1-alpha (MIP-1-alpha). They can be used to reduce susceptibility of hematopoietic cells to a cytotoxic agent, by administering one of the agonist peptides to the cells prior to or during exposure of the cells to the cytotoxic agent. The CXCR4 agonist is used to reduce susceptibility of hematopoietic cells to a cytotoxic agent, particularly in a patient with cancer requiring autologous or allogeneic bone marrow or peripheral blood stem cell transplantation, or an autoimmune disease	
Sequence 31 AA;	
Query Match 93.8%; Score 158.5; DB 5; Length 31;	
Best Local Similarity 96.8%; Pred. No. 4,8e-15;	
Matches 30; Conservative 0; Mismatches 0; Indels 1; Gaps 1;	
1 KPVSLSYRCPCRF-GGGIKMIOEYLEKALN 30	
1 KPVSLSYRCPCRFGGGKMKIOEYLEKALN 31	
RESULT 7	
AAB47702	
AB47702 standard; peptide; 31 AA.	
30-JAN-2002 (first entry)	
SDF-1(1-14) - (G)4 - SDF-1(55-67) -E24/K28-cyclic amide.	
Hematopoietic cell; multiplication; CXCR4 chemokine receptor 4; CXCR4; agonist; stromal cell derived factor one; SDF-1; autoimmune disease; macrophage inflammatory protein 1-alpha; MIP-1-alpha; cancer; autologous; allogeneic; bone marrow; stem cell; transplantation.	
Synthetic.	
Location/Qualifiers	
Modified-site 24.28	
/notes="Joined by side chain cyclization using lactam formation"	

FT	Modified-site	31	/note= "C-terminal amide"
FT			
XX			
XX	WO200176615-A2.		
XX			
XX	18-OCT-2001.		
PD			
XX			
XX	12-APR-2001; 2001WO-CA000540.		
PF			
PR	12-APR-2000; 2000CA-02305036.		
PR	14-SEP-2000; 2000US-0232425P.		
PR	23-FEB-2001; 2001CA-02335109.		
XX			
PA	(UYBR-) UNIV BRITISH COLUMBIA.		
PA	(CHEM-) CHEMOKINE THERAPEUTICS CORP.		
XX			
PI	Salari H, Merzouk A, Arab L, Tudan CR, Saxena G, Eaves CJ;		
PI	Cashman J, Clark-Lewis I,		
XX			
DR	WPI; 2002-025882/03.		
XX			
PT	CXC receptor 4 agonists that reduces hematopoietic cell multiplication		
PT	and susceptibility to cytotoxic agents, are useful for bone marrow or		
PT	peripheral blood stem cell transplantation.		
XX			
PS	Example 1; Page 43; 74pp; English.		
XX			
CC	The sequences given in AAB47680-717 represent peptides which may be used		
CC	in the method of the invention for reducing the rate of hematopoietic		
CC	cell multiplication. These peptides act as CXC chemokine receptor 4		
CC	(CXCR4) agonists to the cells. These peptides are based on stromal cell		
CC	derived factor one (SDF-1) with some also containing sequences derived		
CC	from macrophage inflammatory protein 1-alpha (MIP-1-alpha). They can be		
CC	used to reduce susceptibility of hematopoietic cells to a cytotoxic		
CC	agent, by administering one of the agonist peptides to the cells prior to		
CC	or during exposure of the cells to the cytotoxic agent. The CXCR4 agonist		
CC	is used to reduce susceptibility of hematopoietic cells to a cytotoxic		
CC	agent, particularly in a patient with cancer requiring autologous or		
CC	allogenic bone marrow or peripheral blood stem cell transplantation, or		
CC	an autoimmune disease		
XX			
SO	Sequence 31 AA;		
XX			
Query Match	93.8%;	Score 158.5;	DB 5; Length 31;
Best Local Similarity	96.8%;	Pred. No. 4.6e-15;	
Matches 30; Conservative	0;	Mismatches 0;	Indels 1; Gaps 1;
OY	1 KPVSLSYRCPCRFPGGGLKMIQVLEKALN 30		
DB	1 KPVSLSYRCPCRFPGGGLKMIQVLEKALN 31		
RESULT 8			
ED	AAB47717		
XX	AAB47717 standard; peptide; 31 AA.		
XX			
AC	AAB47717;		
XX			
DT	30-JAN-2002 (first entry)		
XX			
DE	SDF-1(1-14) - (G)4 - SDF-1(55-67)-K20/E24-cyclic amide.		
XX			
KW	Haematopoietic cell; multiplication; CXC chemokine receptor 4; CXCR4;		
KW	agonist; stromal cell derived factor one; SDF-1; autoimmune disease;		
KW	macrophage inflammatory protein 1-alpha; MIP-1-alpha; cancer; autologous;		
KW	allogenic; bone marrow; stem cell; transplantation.		
XX			
OS	Synthetic.		
XX			
TH	Key	Location/Qualifiers	
FT	Modified-site	20..24	
FT	/note= "Joined by side chain cyclization using lactam formation"		

FT		Modified-site	31	/note= "C-terminal amide"
XX				
PN		WO200176615-A2.		
XX				
PD		18-OCT-2001.		
XX				
PF		12-APR-2001; 2001WO-CA000540.		
XX				
PR		12-APR-2000; 2000CA-02305036.		
XX				
PR		14-SEP-2000; 2000US-02324259.		
XX				
PR		23-FEB-2001; 2001CA-02335109.		
XX				
PA		(UYBR-) UNIV BRITISH COLUMBIA.		
XX				
PA		(CHEM-) CHEMOKINE THERAPEUTICS CORP.		
XX				
PI		Salary H, Merzouk A, Arab L, Tudan CR, Saxena G, Eaves CJ;		
XX		Cashman J, Clark-Lewis I;		
DR		WPI; 2002-025882/03.		
XX				
PT		CXC receptor 4 agonists that reduces hematopoietic cell multiplication		
XX		and susceptibility to cytotoxic agents, are useful for bone marrow or		
PT		peripheral blood stem cell transplantation.		
XX				
PS		Example 1; Page 47; 74pp; English.		
XX				
CC		The sequences given in AAB47680-717 represent peptides which may be used		
XX		in the method of the invention for reducing the rate of hematopoietic		
CC		cell multiplication. These peptides act as CXC chemokine receptor 4		
XX		(CXCR4) agonists to the cells. These peptides are based on stromal cell		
CC		derived factor one (SDF-1) with some also containing sequences derived		
XX		from macrophage inflammatory protein 1-alpha (MIP-1-alpha). They can be		
CC		used to reduce susceptibility of hematopoietic cells to a cytotoxic		
XX		agent, by administering one of the agonist peptides to the cells prior to		
CC		or during exposure of the cells to the cytotoxic agent. The CXCR4 agonist		
XX		is used to reduce susceptibility of hematopoietic cells to a cytotoxic		
CC		agent, particularly in a patient with cancer requiring autologous or		
XX		allogeenic bone marrow or peripheral blood stem cell transplantation, or		
CC		an autoimmune disease		
XX				
SQ		Sequence 31 AA;		
OY		Query Match	93.8%	Score 158.5; DB 5; Length 31;
		Best Local Similarity	96.8%;	Pred. No. 4.8e-15;
Dd		Matches 30; Conservative	0;	Mismatches 0; Indels 1; Gaps 1;
		1 KPVSLSYRCPCRF-GGGKMWIOEYLEKALN 30		
		1 KPVSLSYRCPCRFGGGGLKMIOEYLEKALN 31		
RESULT 9				
ID	AAB47715	AAB47715 standard; peptide; 31 AA.		
XX				
AC	AAB47715;			
XX				
DT	30-JAN-2002	(first entry)		
XX				
DE	SDF-1(1-14) - (G)4 - SDF-1(55-67)	amide.		
XX				
KW	Hematopoietic cell; multiplication; CXC chemokine receptor 4; CXCR4;			
XX	agonist; stromal cell derived factor one; SDF-1; autoimmune disease;			
KW	macrophage inflammatory protein 1-alpha; MIP-1-alpha; cancer; autologous;			
XX	allogenic; bone marrow; stem cell; transplantation.			
OS	Synthetic.			
XX				
PH	Key	Location/Qualifiers		
FT	Modified-site	31		
XX		/note= "C-terminal amide"		
XX				

XX	PN	WO200176615-A2.
XX	PD	18-OCT-2001.
XX	PF	12-APR-2001; 2001WO-CA000540.
XX	PR	12-APR-2000; 2000CA-02305036.
XX	PR	14-SEP-2000; 2000US-0232425P.
XX	PR	23-FEB-2001; 2001CA-02335109.
PA	(UTB-R-) UNIV BRITISH COLUMBIA.	
PA	(CHEM-) CHEMOKINE THERAPEUTICS CORP.	
PI	Safari H, Merzouk A, Arab L, Tudan CR, Saxena G, Eaves CJ;	
PI	Cashman J, Clark-Lewis I;	
XX	WPI; 2002-025882/03.	
DR		
XX		
PT	CXC receptor 4 agonists that reduces hematopoietic cell multiplication	
PT	and susceptibility to cytotoxic agents, are useful for bone marrow or	
PT	peripheral blood stem cell transplantation.	
XX		
PS	Example 1; Page 47; 74pp; English.	
XX		
CC	The sequences given in AAB47680-717 represent peptides which may be used	
CC	in the method of the invention for reducing the rate of hematopoietic	
CC	cell multiplication. These peptides act as CXCR4 chemokine receptor 4	
CC	CXCR4 agonists to the cells. These peptides are based on stromal cell	
CC	derived factor one (SDF-1) with some also containing sequences derived	
CC	from macrophage inflammatory protein 1-alpha (MIP-1-alpha). They can be	
CC	used to reduce susceptibility of hematopoietic cells to a cytotoxic	
CC	agent, by administering one of the agonist peptides to the cells prior to	
CC	or during exposure of the cells to the cytotoxic agent. The CXCR4 agonist	
CC	is used to reduce susceptibility of hematopoietic cells to a cytotoxic	
CC	agent, particularly in a patient with cancer requiring autologous or	
CC	allogenic bone marrow or peripheral blood stem cell transplantation, or	
CC	an autoimmune disease	
XX		
XX	Sequence 31 AA;	
QY		
Dd	Query Match 93.8%; Score 158.5; DB 5; Length 31; Best Local Similarity 96.8%; Pred. No. 4.8e-15; Matches 30; Conservative 0; Mismatches 0; Indels 1; Gaps 1,	
OY	1 KPVSLSYRCPCRF-GGGLKWIQYLEKALN 30 1 KPVSLSYRCPCRFGGGLKWIQYLEKALN 31	
RESULT 10		
AAB47707		
ID	AAB47707 standard; peptide; 31 AA.	
AC	AAB47707;	
DT	30-JAN-2002 (first entry)	
DE	SDF-1(1-14) - (G)4 - SDF-1(55-67)-C9/C11-cyclic amide.	
XX		
KV	Hematopoietic cell; multiplication; CXCR4 chemokine receptor 4; CXCR4;	
KV	agonist; stromal cell derived factor one; SDF-1; autoimmune diseases; .	
KW	macrophage inflammatory protein 1-alpha; MIP-1-alpha; cancer; autologous;	
KW	allogenic; bone marrow; stem cell; transplantation.	
OS	Synthetic.	
XX		
FH	Key Location/Qualifiers	
FT	Disulfide-bond 9..11	
FT	Modified-site 31	
XX	/note= "C-terminal amide"	
XX		
XX	WO200176615-A2.	

PD 18-OCT-2001.
XX
XX 12-APR-2001; 2001WO-CA000540.
XX
XX 12-APR-2000; 2000CA-02305036.
PR 14-SEP-2000; 2000US-0232425P.
PR 23-FEB-2001; 2001CA-02335109.
XX
PA (UYBR-) UNIV BRITISH COLUMBIA.
XX (CHEM-) CHEMOKINE THERAPEUTICS CORP.
XX
PI Salari H, Merzouk A, Arab L, Tudan CR, Saxena G, Eaves CJ;
PI Cashman J, Clark-Lewis I;
XX
XX WPI; 2002-025882/03.
XX
XX CXCR4 receptor 4 agonists that reduces hematopoietic cell multiplication
PT and susceptibility to cytotoxic agents, are useful for bone marrow or
PT peripheral blood stem cell transplantation.
XX
XX Example 1; Page 44; 74pp; English.
XX
XX The sequences given in AAB47680-717 represent peptides which may be used
CC in the method of the invention for reducing the rate of hematopoietic
CC cell multiplication. These peptides act as CXCR4 chemokine receptor 4
CC (CXCR4) agonists to the cells. These peptides are based on stromal cell
CC derived factor one (SDF-1) with some also containing sequences derived
CC from macrophage inflammatory protein 1-alpha (MIP-1-alpha). They can be
CC used to reduce susceptibility of hematopoietic cells to a cytotoxic
CC agent, by administering one of the agonist peptides to the cells prior to
CC or during exposure of the cells to the cytotoxic agent. The CXCR4 agonist
CC is used to reduce susceptibility of hematopoietic cells to a cytotoxic
CC agent, particularly in a patient with cancer requiring autologous or
CC allogenic bone marrow or peripheral blood stem cell transplantation, or
CC an autoimmune disease
XX
XX Sequence 31 AA;
SQ
Query Match 93.8%; Score 158.5; DB 5; Length 31;
Best Local Similarity 96.8%; Pred. No. 4.8e-15;
Matches 30; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 1 KPVSLSYRCPCRFP-GGGLKWIQIYLEKALN 30
DB 1 KPVSLSYRCPCRFPGGGGLKWIQIYLEKALN 31
RESULT 11
AAB47716
ID AAB47716 standard; peptide; 31 AA.
XX
XX AAB47716;
AC
XX
DT 30-JAN-2002 (first entry)
XX
XX SDF-1(1-14) - (G)4 - SDF-1(55-67)-E24/K28-cyclic amide.
DE
XX
XX Hematopoietic cell; multiplication; CXCR4 chemokine receptor 4; CXCR4;
KM agonist; stromal cell derived factor one; SDF-1; autoimmune disease;
KW macrophage inflammatory protein 1-alpha; MIP-1-alpha; cancer; autologous;
KW allogenic; bone marrow; stem cell; transplantation.
XX
XX Synthetic.
OS
XX
XX Key Location/Qualifiers
FH Modified-site 24..28
FT /note= "Joined by side chain cyclization using lactam
FT formation"
FT Modified-site 31
FT /note= "C-terminal amide"
XX
XX W0200176615-A2.
XX
XX

PD 18-OCT-2001.
XX
XX 12-APR-2001; 2001WO-CA000540.
XX
XX 12-APR-2000; 2000CA-02305036.
PR 14-SEP-2000; 2000US-0232425P.
PR 23-FEB-2001; 2001CA-02335109.
XX
PA (UYBR-) UNIV BRITISH COLUMBIA.
XX (CHEM-) CHEMOKINE THERAPEUTICS CORP.
XX
PI Salari H, Merzouk A, Arab L, Tudan CR, Saxena G, Eaves CJ;
PI Cashman J, Clark-Lewis I;
XX
XX WPI; 2002-025882/03.
XX
XX CXCR4 receptor 4 agonists that reduces hematopoietic cell multiplication
PT and susceptibility to cytotoxic agents, are useful for bone marrow or
PT peripheral blood stem cell transplantation.
XX
XX Example 1; Page 47; 74pp; English.
XX
XX The sequences given in AAB47680-717 represent peptides which may be used
CC in the method of the invention for reducing the rate of hematopoietic
CC cell multiplication. These peptides act as CXCR4 chemokine receptor 4
CC (CXCR4) agonists to the cells. These peptides are based on stromal cell
CC derived factor one (SDF-1) with some also containing sequences derived
CC from macrophage inflammatory protein 1-alpha (MIP-1-alpha). They can be
CC used to reduce susceptibility of hematopoietic cells to a cytotoxic
CC agent, by administering one of the agonist peptides to the cells prior to
CC or during exposure of the cells to the cytotoxic agent. The CXCR4 agonist
CC is used to reduce susceptibility of hematopoietic cells to a cytotoxic
CC agent, particularly in a patient with cancer requiring autologous or
CC allogenic bone marrow or peripheral blood stem cell transplantation, or
CC an autoimmune disease
XX
XX Sequence 31 AA;
SQ
Query Match 93.8%; Score 158.5; DB 5; Length 31;
Best Local Similarity 96.8%; Pred. No. 4.8e-15;
Matches 30; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 1 KPVSLSYRCPCRFP-GGGLKWIQIYLEKALN 30
DB 1 KPVSLSYRCPCRFPGGGGLKWIQIYLEKALN 31
RESULT 12
AAB47695
ID AAB47695 standard; peptide; 31 AA.
XX
XX AAB47695;
AC
XX
DT 30-JAN-2002 (first entry)
XX
XX SDF-1(1-14) - (G)4 - SDF-1(55-67) amide.
DE
XX
XX Hematopoietic cell; multiplication; CXCR4 chemokine receptor 4; CXCR4;
KM agonist; stromal cell derived factor one; SDF-1; autoimmune disease;
KW macrophage inflammatory protein 1-alpha; MIP-1-alpha; cancer; autologous;
KW allogenic; bone marrow; stem cell; transplantation.
XX
XX Synthetic.
OS
XX
XX Key Location/Qualifiers
FH Modified-site 31
FT /note= "C-terminal amide"
FT
FT W0200176615-A2.
XX
XX 18-OCT-2001.
XX
XX 12-APR-2001; 2001WO-CA000540.
XX
XX

XX 12-APR-2000; 2000CA-02305036.
 PR 14-SEP-2000; 2000US-0232425P.
 PR 23-FEB-2001; 2001CA-02335109.
 XX
 PA (UYBR-) UNIV BRITISH COLUMBIA.
 PA (CHEM-) CHEMOKINE THERAPEUTICS CORP.
 PI Salari H, Merzouk A, Arab L, Tudan CR, Saxena G, Eaves CJ,
 PI Cashman J, Clark-Lewis I;
 DR WPI; 2002-025882/03.
 XX
 PT CXC receptor 4 agonists that reduces hematopoietic cell multiplication
 PT and susceptibility to cytotoxic agents, are useful for bone marrow or
 PT peripheral blood stem cell transplantation.
 XX
 PS Example 1; Page 42; 74pp; English.
 XX
 CC The sequences given in AAB47680-717 represent peptides which may be used
 CC in the method of the invention for reducing the rate of hematopoietic
 CC cell multiplication. These peptides act as CXC chemokine receptor 4
 CC (CXCR4) agonists to the cells. These peptides are based on stromal cell
 CC derived factor one (SDF-1) with some also containing sequences derived
 CC from macrophage inflammatory protein 1-alpha (MIP-1-alpha). They can be
 CC used to reduce susceptibility of hematopoietic cells to a cytotoxic
 CC agent, by administering one of the agonist peptides to the cells prior to
 CC or during exposure of the cells to the cytotoxic agent. The CXCR4 agonist
 CC is used to reduce susceptibility of hematopoietic cells to a cytotoxic
 CC agent, particularly in a patient with cancer requiring autologous or
 CC allogenic bone marrow or peripheral blood stem cell transplantation, or
 CC an autoimmune disease
 XX
 SQ Sequence 31 AA;
 XX
 Query Match 93.8%; Score 158.5; DB 5; Length 31;
 Best Local Similarity 96.8%; Pred. No. 4.8e-15;
 Matches 30; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
 QY 1 KPVSLSYRCPGRPF-GGGLKWIQIYLEKALN 30
 Db 1 KPVSLSYRCPGRPFGGGLKWIQIYLEKALN 31
 XX
 RESULT 13
 AAB47700
 ID AAB47700 standard; peptide; 31 AA.
 XX
 AC AAB47700;
 XX
 DT 30-JAN-2002 (first entry)
 XX
 DE SDF-1(1-14) - (G)4 - SDF-1(55-67)-B24/K28-cyclic acid.
 XX
 KW Haematopoietic cell; multiplication; CXC chemokine receptor 4; CXCR4;
 KW agonist; stromal cell derived factor one; SDF-1; autoimmune disease;
 KW macrophage inflammatory protein 1-alpha; MIP-1-alpha; cancer; autologous;
 KW allogenic; bone marrow; stem cell; transplantation.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 24..28
 FT /note="Joined by side chain cyclization using lactam
 FT formation"
 FT
 XX
 PN WO200176615-A2.
 XX
 PD 18-OCT-2001.
 XX
 PF 12-APR-2001; 2001WO-CA000540.
 XX
 PR 12-APR-2000; 2000CA-02305036.

PR 14-SEP-2000; 2000US-0232425P.
 PR 23-FEB-2001; 2001CA-02335109.
 XX
 PA (UYBR-) UNIV BRITISH COLUMBIA.
 PA (CHEM-) CHEMOKINE THERAPEUTICS CORP.
 PI Salari H, Merzouk A, Arab L, Tudan CR, Saxena G, Eaves CJ,
 PI Cashman J, Clark-Lewis I;
 DR WPI; 2002-025882/03.
 XX
 PT CXC receptor 4 agonists that reduces hematopoietic cell multiplication
 PT and susceptibility to cytotoxic agents, are useful for bone marrow or
 PT peripheral blood stem cell transplantation.
 XX
 PS Example 1; Page 43; 74pp; English.
 XX
 CC The sequences given in AAB47680-717 represent peptides which may be used
 CC in the method of the invention for reducing the rate of hematopoietic
 CC cell multiplication. These peptides act as CXC chemokine receptor 4
 CC (CXCR4) agonists to the cells. These peptides are based on stromal cell
 CC derived factor one (SDF-1) with some also containing sequences derived
 CC from macrophage inflammatory protein 1-alpha (MIP-1-alpha). They can be
 CC used to reduce susceptibility of hematopoietic cells to a cytotoxic
 CC agent, by administering one of the agonist peptides to the cells prior to
 CC or during exposure of the cells to the cytotoxic agent. The CXCR4 agonist
 CC is used to reduce susceptibility of hematopoietic cells to a cytotoxic
 CC agent, particularly in a patient with cancer requiring autologous or
 CC allogenic bone marrow or peripheral blood stem cell transplantation, or
 CC an autoimmune disease
 XX
 SQ Sequence 31 AA;
 XX
 Query Match 93.8%; Score 158.5; DB 5; Length 31;
 Best Local Similarity 96.8%; Pred. No. 4.8e-15;
 Matches 30; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
 QY 1 KPVSLSYRCPGRPF-GGGLKWIQIYLEKALN 30
 Db 1 KPVSLSYRCPGRPFGGGLKWIQIYLEKALN 31
 XX
 RESULT 14
 AAB47703
 ID AAB47703 standard; peptide; 31 AA.
 XX
 AC AAB47703;
 XX
 DT 30-JAN-2002 (first entry)
 XX
 DE SDF-1(1-14) - (G)4 - SDF-1(55-67)-K20/B24-cyclic amide.
 XX
 KW Haematopoietic cell; multiplication; CXC chemokine receptor 4; CXCR4;
 KW agonist; stromal cell derived factor one; SDF-1; autoimmune disease;
 KW macrophage inflammatory protein 1-alpha; MIP-1-alpha; cancer; autologous;
 KW allogenic; bone marrow; stem cell; transplantation.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 20..24
 FT /note="Joined by side chain cyclization using lactam
 FT formation"
 FT Modified-site 31
 FT /note="C-terminal amide"
 FT
 XX
 PN WO200176615-A2.
 XX
 PD 18-OCT-2001.
 XX
 PF 12-APR-2001; 2001WO-CA000540.
 XX
 PR 12-APR-2000; 2000CA-02305036.

```

PR 14-SEP-2000; 2000US-0232425P.
PR 23-FEB-2001; 2001CA-02335109.
XX
XX (UYBR-) UNIV BRITISH COLUMBIA.
PA (CHEM-) CHEMOKINE THERAPEUTICS CORP.
XX
PI Salati H, Merzouk A, Arab L, Tudan CR, Saxena G, Eaves CJ;
PI Cashman J, Clark-Lewis I;
XX
XX WPI; 2002-025882/03.
DR
XX
XX CXC receptor 4 agonists that reduces hematopoietic cell multiplication
PT and susceptibility to cytotoxic agents, are useful for bone marrow or
PT peripheral blood stem cell transplantation.
XX
XX Example 1; Page 43; 74pp; English.
PS
XX
XX The sequences given in AAB47680-717 represent peptides which may be used
CC in the method of the invention for reducing the rate of hematopoietic
CC cell multiplication. These peptides act as CXC chemokine receptor 4
CC (CXCR4) agonists to the cells. These peptides are based on stromal cell
CC derived factor one (SDF-1) with some also containing sequences derived
CC from macrophage inflammatory protein 1-alpha (MIP-1-alpha). They can be
CC used to reduce susceptibility of hematopoietic cells to a cytotoxic
CC agent, by administering one of the agonist peptides to the cells prior to
CC or during exposure of the cells to the cytotoxic agent. The CXCR4 agonist
CC is used to reduce susceptibility of hematopoietic cells to a cytotoxic
CC agent, particularly in a patient with cancer requiring autologous or
CC allogenic bone marrow or peripheral blood stem cell transplantation, or
CC an autoimmune disease
XX
XX Sequence 31 AA;
SQ
XX
XX Query Match 93.8%; Score 158.5; DB 5; Length 31;
XX Best Local Similarity 96.8%; Pred. No. 4.8e-15;
XX Matches 30; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 1 KPVSLSYRCPCRF-GGGLKWIQIYLEKALN 30
DB 1 KPVSLSYRCPCRFGGGLKWIQIYLEKALN 31
XX
XX RESULT 15
XX AAB47714
XX ID AAB47714 standard; peptide; 31 AA.
XX
XX AAB47714;
XX
XX 30-JAN-2002 (first entry)
XX
XX SDF-1(1-14) - (G)4 - SDF-1(55-67) acid.
XX
XX Hematopoietic cell; multiplication; CXC chemokine receptor 4; CXCR4;
XX agonist; stromal cell derived factor one; SDF-1; autoimmune disease;
XX macrophage inflammatory protein 1-alpha; MIP-1-alpha; cancer; autologous;
XX allogenic; bone marrow; stem cell; transplantation.
XX
XX Synthetic.
XX
XX
XX NO200176615-A2.
XX
XX 18-OCT-2001.
XX
XX 12-APR-2001; 2001WO-CA000540.
XX
XX 12-APR-2000; 2000CA-02305036.
XX 14-SEP-2000; 2000US-0232425P.
XX 23-FEB-2001; 2001CA-02335109.
XX
XX (UYBR-) UNIV BRITISH COLUMBIA.
XX (CHEM-) CHEMOKINE THERAPEUTICS CORP.
XX
XX Salati H, Merzouk A, Arab L, Tudan CR, Saxena G, Eaves CJ;
PI

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PI Cashman J, Clark-Lewis I;
XX
XX WPI; 2002-025882/03.
DR
XX
XX CXC receptor 4 agonists that reduces hematopoietic cell multiplication
PT and susceptibility to cytotoxic agents, are useful for bone marrow or
PT peripheral blood stem cell transplantation.
XX
XX Example 1; Page 47; 74pp; English.
PS
XX
XX The sequences given in AAB47680-717 represent peptides which may be used
CC in the method of the invention for reducing the rate of hematopoietic
CC cell multiplication. These peptides act as CXC chemokine receptor 4
CC (CXCR4) agonists to the cells. These peptides are based on stromal cell
CC derived factor one (SDF-1) with some also containing sequences derived
CC from macrophage inflammatory protein 1-alpha (MIP-1-alpha). They can be
CC used to reduce susceptibility of hematopoietic cells to a cytotoxic
CC agent, by administering one of the agonist peptides to the cells prior to
CC or during exposure of the cells to the cytotoxic agent. The CXCR4 agonist
CC is used to reduce susceptibility of hematopoietic cells to a cytotoxic
CC agent, particularly in a patient with cancer requiring autologous or
CC allogenic bone marrow or peripheral blood stem cell transplantation, or
CC an autoimmune disease
XX
XX Sequence 31 AA;
SQ
XX
XX Query Match 93.8%; Score 158.5; DB 5; Length 31;
XX Best Local Similarity 96.8%; Pred. No. 4.8e-15;
XX Matches 30; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 1 KPVSLSYRCPCRF-GGGLKWIQIYLEKALN 30
DB 1 KPVSLSYRCPCRFGGGLKWIQIYLEKALN 31
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XX Search completed: January 4, 2005, 15:46:50
XX Job time : 67.9672 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 4, 2005, 15:43:59 ; Search time 27.0492 Seconds
(without alignments)
73.553 Million cell updates/sec

Title: US-10-086-177a-12

Perfect score: 169

Sequence: 1 KPVSLSTRCPFRFGGLKWIQRYLEKALN 30

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 6631800 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep:*
- 2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep:*
- 3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep:*
- 4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep:*
- 5: /cgn2_6/ptodata/1/1aa/PTUS.COMB.pep:*
- 6: /cgn2_6/ptodata/1/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	158.5	93.8	31	4	US-09-543-940-5
2	138.5	82.0	27	4	US-09-543-940-4
3	132.5	78.4	25	4	US-09-543-940-6
4	118.5	70.1	89	1	US-08-181-556-2
5	118.5	70.1	89	1	US-08-323-084A-1
6	118.5	70.1	89	1	US-08-323-084A-1
7	118.5	70.1	89	1	US-09-461-912A-46
8	118.5	70.1	93	1	US-08-323-084A-5
9	118.5	70.1	93	1	US-08-674-008-5
10	118.5	70.1	93	4	US-09-312-283C-421
11	118.5	70.1	93	4	US-09-919-497-95
12	118.5	70.1	166	4	US-09-646-028-5
13	118.5	70.1	177	4	US-09-646-028-54
14	118.5	70.1	326	3	US-08-808-720-3
15	118.5	70.1	326	3	US-09-467-638-3
16	118.5	70.1	328	3	US-08-808-720-1
17	118.5	70.1	328	3	US-09-467-638-1
18	118.5	70.1	339	4	US-09-646-028-55
19	114.5	67.8	27	4	US-09-543-940-7
20	82	48.5	14	4	US-09-543-940-10
21	69	40.8	13	4	US-09-543-940-9
22	62	36.7	10	4	US-09-543-940-8
23	59.5	35.2	1084	4	US-09-221-013A-8
24	57	33.7	97	4	US-09-270-767-39706
25	57	33.7	97	4	US-09-270-767-54923
26	57	33.7	192	4	US-09-270-767-32013
27	57	33.7	192	4	US-09-270-767-47230

ALIGNMENTS

28	55	32.5	10	4	US-09-543-940-12	Sequence 12, Appl
29	52	30.8	974	3	US-08-960-048-6	Sequence 6, Appl
30	52	30.8	974	4	US-09-838-586-6	Sequence 6, Appl
31	51.5	30.5	504	4	US-09-252-991A-32272	Sequence 32272, A
32	49.5	29.3	535	4	US-09-252-991A-25662	Sequence 25662, A
33	49.5	29.3	588	3	US-08-481-190-16	Sequence 16, Appl
34	49.5	29.3	588	5	PCT-US93-00869-16	Sequence 16, Appl
35	49.5	29.3	1129	4	US-09-023-905A-2	Sequence 2, Appl
36	49.5	29.3	1151	4	US-09-023-905A-4	Sequence 4, Appl
37	49	29.0	416	1	US-08-117-083-61	Sequence 61, Appl
38	48.5	28.7	685	3	US-08-960-048-7	Sequence 7, Appl
39	48.5	28.7	685	4	US-09-838-586-7	Sequence 7, Appl
40	48	28.4	436	4	US-09-252-991A-28555	Sequence 28555, A
41	48	28.4	542	4	US-09-489-039A-8620	Sequence 8620, Ap
42	47.5	28.1	305	4	US-09-252-991A-26204	Sequence 26204, A
43	47.5	28.1	927	4	US-09-252-991A-20340	Sequence 20340, A
44	47	27.8	22	4	US-09-762-724-25	Sequence 25, Appl
45	47	27.8	71	4	US-09-270-767-56665	Sequence 56665, A

RESULT 1
US-09-543-940-5
Sequence 5, Application US/09543940
Patent No. 6613742
GENERAL INFORMATION:
APPLICANT: Huang, Ziwei
APPLICANT: Luo, Zhaoen
APPLICANT: Zhou, Naiming
TITLE OF INVENTION: Chemokine-Derived Synthetic Peptides
FILE REFERENCE: 8321-40
CURRENT APPLICATION NUMBER: US/09/543,940
CURRENT FILING DATE: 2000-04-06
PRIOR APPLICATION NUMBER: 60/128,106
PRIOR FILING DATE: 1999-04-07
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 5
LENGTH: 31
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURES:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: peptide containing segments from N- and C-terminal
US-09-543-940-5
Query Match 93.8%; Score 158.5; DB 4; Length 31;
Best Local Similarity 96.8%; Pred. No. 2.6e-15;
Matches 30; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 1 KPVSLSTRCPFRFGGLKWIQRYLEKALN 30
DB 1 KPVSLSTRCPFRFGGLKWIQRYLEKALN 31
RESULT 2
US-09-543-940-4
Sequence 4, Application US/09543940
Patent No. 6613742
GENERAL INFORMATION:
APPLICANT: Huang, Ziwei
APPLICANT: Luo, Zhaoen
APPLICANT: Zhou, Naiming
TITLE OF INVENTION: Chemokine-Derived Synthetic Peptides
FILE REFERENCE: 8321-40
CURRENT APPLICATION NUMBER: US/09/543,940
CURRENT FILING DATE: 2000-04-06
PRIOR APPLICATION NUMBER: 60/128,106

PRIOR FILING DATE: 1999-04-07
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentln Ver. 2.1
SEQ ID NO 4
LENGTH: 27
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: peptide containing segments from N- and C-terminal
OTHER INFORMATION: regions of human SDF-1 protein
US-09-543-940-4

Query Match 82.0%; Score 138.5; DB 4; Length 27;
Best Local Similarity 96.3%; Pred. No. 1.4e-12;
Matches 26; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 5 LSYRCPFRFGGGLKMWIOEYLEKALN 30
DB 1 LSYRCPFRFGGGLKMWIOEYLEKALN 27

RESULT 3
US-09-543-940-6
Sequence 6, Application US/09543940
Patent No. 6613742
GENERAL INFORMATION:
APPLICANT: Huang, Ziwei
APPLICANT: Luo, Zhaoen
APPLICANT: Zhou, Naiming
APPLICANT: Luo, Jiansong
TITLE OF INVENTION: Chemokine-Derived Synthetic Peptides
FILE REFERENCE: 8321-40
CURRENT APPLICATION NUMBER: US/09/543,940
PRIOR FILING DATE: 2000-04-06
PRIOR APPLICATION NUMBER: 60/128,106
PRIOR FILING DATE: 1999-04-07
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentln Ver. 2.1
SEQ ID NO 6
LENGTH: 25
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: peptide containing segments from N- and C-terminal
OTHER INFORMATION: regions of human SDF-1 protein
US-09-543-940-6

Query Match 78.4%; Score 132.5; DB 4; Length 25;
Best Local Similarity 96.2%; Pred. No. 8.8e-12;
Matches 25; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 5 LSYRCPFRFGGGLKMWIOEYLEKALN 30
DB 1 LSYRCPFRFGGGLKMWIOEYLEKALN 25

RESULT 4
US-08-181-556-2
Sequence 2, Application US/08181556
Patent No. 5525486
GENERAL INFORMATION:
APPLICANT: HONTO, Tasuku
APPLICANT: TASHIRO, Kei
APPLICANT: TADA, Hideaki
TITLE OF INVENTION: PROCESS FOR CONSTRUCTING CDNA LIBRARY,
TITLE OF INVENTION: AND NOVEL POLYPEPTIDE AND DNA CODING FOR THE SAME
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: STEVENS, DAVIS, MILLER & MOSHER
STREET: 515 No. 5525486th Washington Street (P.O. Box 1427)
CITY: Alexandria

STATE: Virginia
COUNTRY: USA
ZIP: 22313
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Releasee #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/181,556
FILING DATE: 14-JAN-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 5-22098
FILING DATE: 14-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: POULOS III, James A.
REGISTRATION NUMBER: 31714
REFERENCE//DOCKET NUMBER: TP/29088
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 549-7200
TELEFAX: (703) 528-5313
TELEX: 89-2746
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 89 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-181-556-2

Query Match 70.1%; Score 118.5; DB 1; Length 89;
Best Local Similarity 40.3%; Pred. No. 2.9e-09;
Matches 27; Conservative 0; Mismatches 3; Indels 37; Gaps 1;

QY 1 KPVSLSYRCPFRFGG-----GLKWIQ 23
DB 22 KPVSLSYRCPFRFGGSHIAPANYKILNTPNCALQIVARLKNNNRQVCIDPKWKIQ 81

QY 24 YLEKALN 30
DB 82 YLEKALN 88

RESULT 5
US-08-323-084A-1
Sequence 1, Application US/08323084A
Patent No. 5563048
GENERAL INFORMATION:
APPLICANT: HONTO, TASUKU
APPLICANT: SHIROZU, MICHIO
APPLICANT: TADA, HIDEAKI
TITLE OF INVENTION: No. 5563048el Polypeptides and DNAs encoding them
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: SUGHRUE, MITON, ZINN, MACPEAK & SEAS
STREET: 2100 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20037-3202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Releasee #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/323,084A
FILING DATE: 14-OCT-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 280505/1993
FILING DATE: 14-OCT-1993

```
TELECOMMUNICATION INFORMATION:
:
: TELEPHONE: (202)293-7060
: TELEFAX: (202)293-7860
:
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
:   LENGTH: 89 amino acids
:   TYPE: amino acid
:   TOPOLOGY: linear
: MOLECULE TYPE: protein
:
: US-08-323-084A-1

Query Match      70.1%; Score 118.5; DB 1; Length 89;
Best Local Similarity 40.3%; Pred. No. 2.9e-09;
Matches 27; Conservative 0; Mismatches 3; Indels 37; Gaps 1;

QY 1 KPVSLSYRCPCRFPGG-----GLKXIOE 23
DB 22 KPVSLSYRCPCRFESHVARANVHKLINTPNCALQIVARLKNNNRQVCIDPRLKXIOE 81
QY 24 YLEKALN 30
DB 82 YLEKALN 88

RESULT 6
US-08-674-008-1
: Sequence 1, Application US/08674008
: Patent No. 5756084
: GENERAL INFORMATION:
: APPLICANT: HONJO, Tasaku
: APPLICANT: SHIROZU, Michio
: APPLICANT: TADA, Hideaki
: TITLE OF INVENTION: HUMAN STROMAL DERIVED
: TITLE OF INVENTION: FACTOR 1 AND 1 (As Amended)
: NUMBER OF SEQUENCES: 20
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS
: STREET: 2100 Pennsylvania Avenue, N.W.
: CITY: Washington
: STATE: D.C.
: COUNTRY: U.S.A.
: ZIP: 20037-3202
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/674,008
: FILING DATE: 1-JUL-1996
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/323,084
: FILING DATE: 14-OCT-1994
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: JP 280505/1993
: FILING DATE: 14-OCT-1993
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (202)293-7060
: TELEFAX: (202)293-7860
:
: TELEX: 6491103
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
:   LENGTH: 89 amino acids
:   TYPE: amino acid
:   TOPOLOGY: linear
: MOLECULE TYPE: protein
:
: US-08-674-008-1

Query Match      70.1%; Score 118.5; DB 1; Length 89;
Best Local Similarity 40.3%; Pred. No. 2.9e-09;
Matches 27; Conservative 0; Mismatches 3; Indels 37; Gaps 1;
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QY 1 KPVSLSYRCPCRFPGG-----GLKXIOE 23
DB 22 KPVSLSYRCPCRFESHVARANVHKLINTPNCALQIVARLKNNNRQVCIDPRLKXIOE 81
QY 24 YLEKALN 30
DB 82 YLEKALN 88

RESULT 7
US-09-461-912A-46
: Sequence 46, Application US/09461912A
: Patent No. 6708655
: GENERAL INFORMATION:
: APPLICANT: Stanton, Lawrence A.
: APPLICANT: White, R. Tyler
: APPLICANT: Damm, Deborah L.
: APPLICANT: Lewicki, John A.
: TITLE OF INVENTION: Methods for detection and use of
: FILE REFERENCE: SCIOS.011A
: CURRENT FILING DATE: 1999-12-15
: PRIOR APPLICATION NUMBER: US 60/113,008
: PRIOR FILING DATE: 1998-12-18
: NUMBER OF SEQ ID NOS: 48
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 46
: LENGTH: 89
: TYPE: PRT
: ORGANISM: Homo sapiens
:
: US-09-461-912A-46

Query Match      70.1%; Score 118.5; DB 4; Length 89;
Best Local Similarity 40.3%; Pred. No. 2.9e-09;
Matches 27; Conservative 0; Mismatches 3; Indels 37; Gaps 1;

QY 1 KPVSLSYRCPCRFPGG-----GLKXIOE 23
DB 22 KPVSLSYRCPCRFESHVARANVHKLINTPNCALQIVARLKNNNRQVCIDPRLKXIOE 81
QY 24 YLEKALN 30
DB 82 YLEKALN 88

RESULT 8
US-08-323-084A-5
: Sequence 5, Application US/08323084A
: Patent No. 5563048
: GENERAL INFORMATION:
: APPLICANT: HONJO, TASUKU
: APPLICANT: SHIROZU, MICHIO
: APPLICANT: TADA, HIDEAKI
: TITLE OF INVENTION: No. 5563048e1 Polypeptides and DNAs encoding them
: NUMBER OF SEQUENCES: 20
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS
: STREET: 2100 Pennsylvania Avenue, N.W.
: CITY: Washington
: STATE: D.C.
: COUNTRY: U.S.A.
: ZIP: 20037-3202
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/323,084A
: FILING DATE:
: CLASSIFICATION: 435
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 280505/1993
FILING DATE: 14-OCT-1993
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)293-7060
TELEFAX: (202)293-7860
TELEX: 6491103
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 93 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-323-084A-5

Query Match 70.1%; Score 118.5; DB 1; Length 93;
Best Local Similarity 40.3%; Pred. No. 3e-09;
Matches 27; Conservative 0; Mismatches 3; Indels 37; Gaps 1;

QY 1 KPVSLSYRCPCRFPGG-----GLKWIQE 23
Db 22 KPVSLSYRCPCRFESHVARANVHKILNTPNCALQIVARLKNRRQVCIDPKLKWIOE 81
QY 24 YLEKALN 30
Db 82 YLEKALN 88

RESULT 9
US-08-674-008-5
Sequence 5, Application US/08674008
Patent No. 5756084
GENERAL INFORMATION:
APPLICANT: HONJO, Tasaku
APPLICANT: SHIROZU, Michio
APPLICANT: TADA, Hideaki
TITLE OF INVENTION: HUMAN STROMAL DERIVED
TITLE OF INVENTION: FACTOR 1' AND 1 (As Amended)
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS
STREET: 2100 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20037-3202
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/674,008
FILING DATE: 1-JUL-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/323,084
FILING DATE: 14-OCT-1994
PRIOR APPLICATION DATA: JP 280505/1993
FILING DATE: 14-OCT-1993
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)293-7060
TELEFAX: (202)293-7860
TELEX: 6491103
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 93 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-674-008-5

Query Match 70.1%; Score 118.5; DB 1; Length 93;
Best Local Similarity 40.3%; Pred. No. 3e-09;
Matches 27; Conservative 0; Mismatches 3; Indels 37; Gaps 1;

QY 1 KPVSLSYRCPCRFPGG-----GLKWIQE 23
Db 22 KPVSLSYRCPCRFESHVARANVHKILNTPNCALQIVARLKNRRQVCIDPKLKWIOE 81

QY 24 YLEKALN 30
Db 82 YLEKALN 88

RESULT 10
US-09-312-283C-421
Sequence 421, Application US/09312283C
Patent No. 6573095
GENERAL INFORMATION:
APPLICANT: Watson, James D.
APPLICANT: Strachan, Lorna
APPLICANT: Sleeman, Matthew
APPLICANT: Ormset, Rene
APPLICANT: Murison, James G.
APPLICANT: Kumble, Krishanand D.
TITLE OF INVENTION: Compositions Isolated from Skin Cells
TITLE OF INVENTION: and Methods for Their Use
FILE REFERENCE: 11000.1011c2
CURRENT APPLICATION NUMBER: US/09/312,283C
CURRENT FILING DATE: 1999-05-14
NUMBER OF SEQ ID NOS: 425
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 421
LENGTH: 93
TYPE: PRT
ORGANISM: Mouse
US-09-312-283C-421

Query Match 70.1%; Score 118.5; DB 4; Length 93;
Best Local Similarity 40.3%; Pred. No. 3e-09;
Matches 27; Conservative 0; Mismatches 3; Indels 37; Gaps 1;

QY 1 KPVSLSYRCPCRFPGG-----GLKWIQE 23
Db 22 KPVSLSYRCPCRFESHVARANVHKILNTPNCALQIVARLKNRRQVCIDPKLKWIOE 81
QY 24 YLEKALN 30
Db 82 YLEKALN 88

RESULT 11
US-09-919-497-95
Sequence 95, Application US/09919497
Patent No. 6773883
GENERAL INFORMATION:
APPLICANT: Mutter, George L.
TITLE OF INVENTION: PROGNOSTIC CLASSIFICATION OF ENDOMETRIAL CANCER
FILE REFERENCE: B0801/7725
CURRENT APPLICATION NUMBER: US/09/919,497
CURRENT FILING DATE: 2001-07-31
PRIOR APPLICATION NUMBER: US 60/221,735
PRIOR FILING DATE: 2000-07-31
NUMBER OF SEQ ID NOS: 100
SOFTWARE: Patentin version 3.0
SEQ ID NO 95
LENGTH: 93
TYPE: PRT
ORGANISM: Homo sapiens
US-09-919-497-95

Query Match 70.1%; Score 118.5; DB 4; Length 93;
Best Local Similarity 40.3%; Pred. No. 3e-09;
Matches 27; Conservative 0; Mismatches 3; Indels 37; Gaps 1;

QY 1 KPVSLSYRCPCRFPGG-----GLKXIOE 23
Db 22 KPVSLSYRCPCRFESHVARANVGHILKILNTPNCALQIVARLKNNNRQVCIDPRLKXIOE 81
QY 24 YLEKALN 30
Db 82 YLEKALN 88

RESULT 12

US-09-646-028-5
; Sequence 5, Application US/09646028
; Patent No. 6562347
; GENERAL INFORMATION:
; APPLICANT: Kwak, Larry
; APPLICANT: Birsayn, Arya
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF
; FILE REFERENCE: 14014.0316/P
; CURRENT APPLICATION NUMBER: US/09/646,028
; PRIOR FILING DATE: 2000-09-12
; PRIOR APPLICATION NUMBER: 60/077,745
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of artificial sequence:/note=synthetic construct
US-09-646-028-5

Query Match 70.1%; Score 118.5; DB 4; Length 166;
Best Local Similarity 40.3%; Pred. No. 5.4e-09;
Matches 27; Conservative 0; Mismatches 3; Indels 37; Gaps 1;

QY 1 KPVSLSYRCPCRFPGG-----GLKXIOE 23
Db 22 KPVSLSYRCPCRFESHVARANVGHILKILNTPNCALQIVARLKNNNRQVCIDPRLKXIOE 81
QY 24 YLEKALN 30
Db 82 YLEKALN 88

RESULT 13

US-09-646-028-54
; Sequence 54, Application US/09646028
; Patent No. 6562347
; GENERAL INFORMATION:
; APPLICANT: Kwak, Larry
; APPLICANT: Birsayn, Arya
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF
; FILE REFERENCE: 14014.0316/P
; CURRENT APPLICATION NUMBER: US/09/646,028
; PRIOR FILING DATE: 2000-09-12
; PRIOR APPLICATION NUMBER: 60/077,745
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 54
; LENGTH: 177
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of artificial sequence:/note=synthetic construct
US-09-646-028-54

Query Match 70.1%; Score 118.5; DB 4; Length 177;
Best Local Similarity 40.3%; Pred. No. 5.7e-09;

Matches 27; Conservative 0; Mismatches 3; Indels 37; Gaps 1;
QY 1 KPVSLSYRCPCRFPGG-----GLKXIOE 23
Db 4 KPVSLSYRCPCRFESHVARANVGHILKILNTPNCALQIVARLKNNNRQVCIDPRLKXIOE 63
QY 24 YLEKALN 30
Db 64 YLEKALN 70

RESULT 14

US-08-808-720-3
; Sequence 3, Application US/08808720
; Patent No. 6100387
; GENERAL INFORMATION:
; APPLICANT: Herrmann, Steve
; APPLICANT: Swenberg, Stephen
; TITLE OF INVENTION: CHIMERIC POLYPEPTIDES CONTAINING
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; STREET: 87 Cambridgepark
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/808,720
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Sprunger, Suzanne
; REGISTRATION NUMBER: P-41,323
; REFERENCE/DOCKET NUMBER: G15291
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8284
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 326 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-808-720-3

Query Match 70.1%; Score 118.5; DB 3; Length 326;
Best Local Similarity 40.3%; Pred. No. 1.1e-08;
Matches 27; Conservative 0; Mismatches 3; Indels 37; Gaps 1;

QY 1 KPVSLSYRCPCRFPGG-----GLKXIOE 23
Db 20 KPVSLSYRCPCRFESHVARANVGHILKILNTPNCALQIVARLKNNNRQVCIDPRLKXIOE 79
QY 24 YLEKALN 30
Db 80 YLEKALN 86

RESULT 15

US-09-467-638-3
; Sequence 3, Application US/09467638
; Patent No. 6730296
; GENERAL INFORMATION:
; APPLICANT: Herrmann, Steve
; APPLICANT: Swenberg, Stephen

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; TITLE OF INVENTION: CHIMERIC POLYPEPTIDES CONTAINING
; TITLE OF INVENTION: CHEMOKINE DOMAINS
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 Cambridgepark
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02140
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/467,638
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/808,720
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Sprunger, Suzanne
; REGISTRATION NUMBER: P-41,323
; REFERENCE/DOCKET NUMBER: G15291
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8284
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 326 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
; US-09-467-638-3

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Query Match 70.1%; Score 118.5; DB 4; Length 326;
Best Local Similarity 40.3%; Pred. No. 1.1e-06;
Matches 27; Conservative 0; Mismatches 3; Indels 37; Gaps 1;

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QY 1 KPVSLSTRCPGRFPG-----GLKWIQ 23
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Db 20 KPVSLSTRCPGRFESHVARANVGLKILNTPNCALQIVARLKNNRQVCIDPKLWIQ 79
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QY 24 YLEKALN 30
    |||||
Db 80 YLEKALN 86

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Search completed: January 4, 2005, 15:47:49
 Job time : 30.0492 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 4, 2005, 15:46:58 ; Search time 97.8689 Seconds
(without alignments)
110.268 Million cell updates/sec

Title: US-10-086-177A-12

Perfect score: 169
Sequence: 1 KPVSLSYRCPCRFPGGLKWIQRYLEKALN 30

Scoring table: BLOSUM62
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Searched: 1599051 seqs, 359727711 residues

Total number of hits satisfying chosen parameters: 1599051

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications AA:*

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- 2: /cgn2_6/prodata/1/pubppa/PCT_NEW_PUB.pep:*
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- 12: /cgn2_6/prodata/1/pubppa/US09_NEW_PUB.pep:*
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- 14: /cgn2_6/prodata/1/pubppa/US10B_PUBCOMB.pep:*
- 15: /cgn2_6/prodata/1/pubppa/US10C_PUBCOMB.pep:*
- 16: /cgn2_6/prodata/1/pubppa/US10D_PUBCOMB.pep:*
- 17: /cgn2_6/prodata/1/pubppa/US10_NEW_PUB.pep:*
- 18: /cgn2_6/prodata/1/pubppa/US11_NEW_PUB.pep:*
- 19: /cgn2_6/prodata/1/pubppa/US60_NEW_PUB.pep:*
- 20: /cgn2_6/prodata/1/pubppa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	169	100.0	30 9 US-09-835-107-12	Sequence 12, Appl
2	169	100.0	30 9 US-09-835-107-14	Sequence 14, Appl
3	169	100.0	30 14 US-10-086-177A-12	Sequence 12, Appl
4	169	100.0	30 14 US-10-086-177A-14	Sequence 14, Appl
5	158.5	93.8	31 9 US-09-835-107-13	Sequence 13, Appl
6	158.5	93.8	31 9 US-09-835-107-15	Sequence 15, Appl
7	158.5	93.8	31 9 US-09-835-107-20	Sequence 20, Appl
8	158.5	93.8	31 9 US-09-835-107-21	Sequence 21, Appl
9	158.5	93.8	31 9 US-09-835-107-22	Sequence 22, Appl
10	158.5	93.8	31 9 US-09-835-107-23	Sequence 23, Appl
11	158.5	93.8	31 9 US-09-835-107-26	Sequence 26, Appl
12	158.5	93.8	31 9 US-09-835-107-27	Sequence 27, Appl
13	158.5	93.8	31 14 US-10-086-177A-13	Sequence 13, Appl

14	158.5	93.8	31 14 US-10-086-177A-15	Sequence 15, Appl
15	158.5	93.8	31 14 US-10-086-177A-20	Sequence 20, Appl
16	158.5	93.8	31 14 US-10-086-177A-21	Sequence 21, Appl
17	158.5	93.8	31 14 US-10-086-177A-22	Sequence 22, Appl
18	158.5	93.8	31 14 US-10-086-177A-23	Sequence 23, Appl
19	158.5	93.8	31 14 US-10-086-177A-26	Sequence 26, Appl
20	158.5	93.8	31 14 US-10-086-177A-27	Sequence 27, Appl
21	157.5	93.2	33 9 US-09-835-107-16	Sequence 16, Appl
22	157.5	93.2	33 9 US-09-835-107-18	Sequence 18, Appl
23	157.5	93.2	33 14 US-10-086-177A-16	Sequence 16, Appl
24	157.5	93.2	33 14 US-10-086-177A-18	Sequence 18, Appl
25	157	92.9	34 9 US-09-835-107-17	Sequence 17, Appl
26	157	92.9	34 9 US-09-835-107-19	Sequence 19, Appl
27	157	92.9	34 14 US-10-086-177A-17	Sequence 17, Appl
28	157	92.9	34 14 US-10-086-177A-19	Sequence 19, Appl
29	155.5	92.0	31 9 US-09-835-107-24	Sequence 24, Appl
30	155.5	92.0	31 9 US-09-835-107-25	Sequence 25, Appl
31	155.5	92.0	31 14 US-10-086-177A-24	Sequence 24, Appl
32	155.5	92.0	31 14 US-10-086-177A-25	Sequence 25, Appl
33	149.5	88.5	31 9 US-09-852-424-122	Sequence 122, Appl
34	149.5	88.5	31 9 US-09-852-424-124	Sequence 124, Appl
35	149.5	88.5	31 9 US-09-852-424-123	Sequence 123, Appl
36	149.5	88.5	31 9 US-09-852-424-134	Sequence 134, Appl
37	149.5	88.5	31 9 US-09-852-424-135	Sequence 135, Appl
38	149.5	88.5	31 9 US-09-852-424-75	Sequence 75, Appl
39	148	87.6	34 9 US-09-852-424-123	Sequence 123, Appl
40	148	87.6	34 9 US-09-852-424-125	Sequence 125, Appl
41	148	87.6	34 9 US-09-852-424-95	Sequence 95, Appl
42	144.5	85.1	31 9 US-09-852-424-79	Sequence 79, Appl
43	144.5	85.5	31 9 US-09-852-424-94	Sequence 94, Appl
44	144.5	85.5	31 9 US-09-852-424-99	Sequence 99, Appl
45	144	85.2	34 9 US-09-852-424-99	Sequence 99, Appl

ALIGNMENTS

RESULT 1
US-09-835-107-12
Sequence 12, Application US/09835107
Patent No. US20020165123A1
GENERAL INFORMATION:
APPLICANT: Tudan, Christopher R.
APPLICANT: Merzouk, Ahmed
APPLICANT: Arab, Lakhdar
APPLICANT: Saxena, Geeta
APPLICANT: Raves, Connie J.
APPLICANT: Cashman, Johanne
APPLICANT: Clark-Lewis
APPLICANT: Salati, Hassan
TITLE OF INVENTION: CXCR4 AGONIST TREATMENT OF HEMATOPOIETIC CELLS
FILE REFERENCE: SMAR012
CURRENT APPLICATION NUMBER: US/09/835,107
CURRENT FILING DATE: 2001-08-20
PRIOR APPLICATION NUMBER: CA 2,305,036
PRIOR FILING DATE: 2000-04-12
PRIOR APPLICATION NUMBER: US 60/232,425
PRIOR FILING DATE: 2000-09-14
PRIOR APPLICATION NUMBER: CA 2,335,109
PRIOR FILING DATE: 2001-02-23
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 12
LENGTH: 30
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURES:
NAME/KEY: DOMAIN
LOCATION: (15)..(17)
OTHER INFORMATION: spacer monomers (such as the illustrated glycine
OTHER INFORMATION: G's) may be used in variable numbers, such as 2, 3
OTHER INFORMATION: or 4 glycines.
OTHER INFORMATION: Synthesised in Laboratory:

OTHER INFORMATION: SDF-1(1-14) - (G)3-SDF-1(55-67) acid
US-09-835-107-12

Query Match 100.0%; Score 169; DB 9; Length 30;
Best Local Similarity 100.0%; Pred. No. 4.8e-16;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPVSLSYRCPCRFPGGGLKWIQEYLEKALN 30
DB 1 KPVSLSYRCPCRFPGGGLKWIQEYLEKALN 30

RESULT 2

US-09-835-107-14
Sequence 14, Application US/09835107
Patent No. US20020165123A1
GENERAL INFORMATION:
APPLICANT: Tudan, Christopher R.
APPLICANT: Merzouk, Ahmed
APPLICANT: Arab, Lakhdar
APPLICANT: Saxena, Geeta
APPLICANT: Eaves, Connie J.
APPLICANT: Cashman, Johanne
APPLICANT: Clark-Lewis
APPLICANT: Salari, Hassan
TITLE OF INVENTION: CXCR4 AGONIST TREATMENT OF HEMATOPOIETIC CELLS
FILE REFERENCE: SMAR012
CURRENT APPLICATION NUMBER: US/09/835,107
CURRENT FILING DATE: 2001-08-20
PRIOR APPLICATION NUMBER: CA 2,305,036
PRIOR FILING DATE: 2000-04-12
PRIOR APPLICATION NUMBER: US 60/232,425
PRIOR FILING DATE: 2000-09-14
PRIOR APPLICATION NUMBER: CA 2,335,109
PRIOR FILING DATE: 2001-02-23
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 14
LENGTH: 30
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: DOMAIN
LOCATION: (15)..(17)
OTHER INFORMATION: spacer monomers (such as the illustrated glycine
OTHER INFORMATION: C's) may be used in variable numbers, such as 2, 3
OTHER INFORMATION: or 4 glycines.
OTHER INFORMATION: Synthesized in Laboratory:
NAME/KEY: MOD RES
LOCATION: (30)
OTHER INFORMATION: AMIDATION
US-09-835-107-14

Query Match 100.0%; Score 169; DB 9; Length 30;
Best Local Similarity 100.0%; Pred. No. 4.8e-16;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPVSLSYRCPCRFPGGGLKWIQEYLEKALN 30
DB 1 KPVSLSYRCPCRFPGGGLKWIQEYLEKALN 30

RESULT 3

US-10-086-177A-12
Sequence 12, Application US/10086177A
Publication No. US20030148940A1
GENERAL INFORMATION:
APPLICANT: Tudan, Christopher R.
APPLICANT: Merzouk, Ahmed
APPLICANT: Saxena, Geeta
APPLICANT: Eaves, Connie J.
APPLICANT: Cashman, Johanne

APPLICANT: Clark-Lewis, Ian
APPLICANT: Salari, Hassan
TITLE OF INVENTION: CXCR Agonist Treatment of Hematopoietic
TITLE OF INVENTION: Cells
FILE REFERENCE: SMAR-012CIP
CURRENT APPLICATION NUMBER: US/10/086,177A
CURRENT FILING DATE: 2002-02-26
PRIOR APPLICATION NUMBER: 09/835,107
PRIOR FILING DATE: 2001-04-12
PRIOR APPLICATION NUMBER: 60/232,425
PRIOR FILING DATE: 2000-09-14
PRIOR APPLICATION NUMBER: CA 2,305,036
PRIOR FILING DATE: 2000-04-12
PRIOR APPLICATION NUMBER: CA 2,335,109
PRIOR FILING DATE: 2001-02-23
NUMBER OF SEQ ID NOS: 34
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 12
LENGTH: 30
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthesized in Laboratory: SDF-1 (1-14) - (G)
US-10-086-177A-12

Query Match 100.0%; Score 169; DB 14; Length 30;
Best Local Similarity 100.0%; Pred. No. 4.8e-16;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPVSLSYRCPCRFPGGGLKWIQEYLEKALN 30
DB 1 KPVSLSYRCPCRFPGGGLKWIQEYLEKALN 30

RESULT 4

US-10-086-177A-14
Sequence 14, Application US/10086177A
Publication No. US20030148940A1
GENERAL INFORMATION:
APPLICANT: Tudan, Christopher R.
APPLICANT: Merzouk, Ahmed
APPLICANT: Saxena, Geeta
APPLICANT: Eaves, Connie J.
APPLICANT: Cashman, Johanne
APPLICANT: Clark-Lewis, Ian
APPLICANT: Salari, Hassan
TITLE OF INVENTION: CXCR Agonist Treatment of Hematopoietic
TITLE OF INVENTION: Cells
FILE REFERENCE: SMAR-012CIP
CURRENT APPLICATION NUMBER: US/10/086,177A
CURRENT FILING DATE: 2002-02-26
PRIOR APPLICATION NUMBER: 09/835,107
PRIOR FILING DATE: 2001-04-12
PRIOR APPLICATION NUMBER: 60/232,425
PRIOR FILING DATE: 2000-09-14
PRIOR APPLICATION NUMBER: CA 2,305,036
PRIOR FILING DATE: 2000-04-12
PRIOR APPLICATION NUMBER: CA 2,335,109
PRIOR FILING DATE: 2001-02-23
NUMBER OF SEQ ID NOS: 34
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 14
LENGTH: 30
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthesized in Laboratory: SDF-1 (1-14) - (G)
US-10-086-177A-14

Query Match 100.0%; Score 169; DB 14; Length 30;
Best Local Similarity 100.0%; Pred. No. 4.8e-16;

Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KPVSLSYRCPCRFPGGGLKMIQIYLEYKALN 30
Db 1 KPVSLSYRCPCRFPGGGLKMIQIYLEYKALN 30

RESULT 5

US-09-835-107-13
Sequence 13, Application US/09835107
Patent No. US20020165123A1
GENERAL INFORMATION:
APPLICANT: Tudan, Christopher R.
APPLICANT: Merzouk, Ahmed
APPLICANT: Arab, Lakhdar
APPLICANT: Saxena, Geeta
APPLICANT: Bayes, Connie J.
APPLICANT: Cashman, Johanne
APPLICANT: Clark-Lewis
APPLICANT: Salari, Hassan
TITLE OF INVENTION: CXCR4 AGONIST TREATMENT OF HEMATOPOIETIC CELLS
FILE REFERENCE: SMAR012
CURRENT APPLICATION NUMBER: US/09/835,107
CURRENT FILING DATE: 2001-08-20
PRIOR APPLICATION NUMBER: CA 2,305,036
PRIOR FILING DATE: 2000-04-12
PRIOR APPLICATION NUMBER: US 60/232,425
PRIOR FILING DATE: 2000-09-14
PRIOR APPLICATION NUMBER: CA 2,335,109
PRIOR FILING DATE: 2001-02-23
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 13
LENGTH: 31
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURES:
NAME/KEY: DOMAIN
LOCATION: (16)..(19)
OTHER INFORMATION: spacer monomers (such as the illustrated glycine
OTHER INFORMATION: G's) may be used in variable numbers, such as 2, 3
OTHER INFORMATION: Synthesised in Laboratory:
OTHER INFORMATION: SDF-1(1-14)-(G)4-SDF-1(55-67) acid: or CTCB0013
US-09-835-107-13

Query Match 93.8%; Score 158.5; DB 9; Length 31;

Best Local Similarity 96.8%; Pred. No. 1.4e-14;
Matches 30; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 KPVSLSYRCPCRFPGGGLKMIQIYLEYKALN 30
Db 1 KPVSLSYRCPCRFPGGGLKMIQIYLEYKALN 31

RESULT 6

US-09-835-107-15
Sequence 15, Application US/09835107
Patent No. US20020165123A1
GENERAL INFORMATION:
APPLICANT: Tudan, Christopher R.
APPLICANT: Merzouk, Ahmed
APPLICANT: Arab, Lakhdar
APPLICANT: Saxena, Geeta
APPLICANT: Bayes, Connie J.
APPLICANT: Cashman, Johanne
APPLICANT: Clark-Lewis
APPLICANT: Salari, Hassan
TITLE OF INVENTION: CXCR4 AGONIST TREATMENT OF HEMATOPOIETIC CELLS
FILE REFERENCE: SMAR012
CURRENT APPLICATION NUMBER: US/09/835,107
CURRENT FILING DATE: 2001-08-20
PRIOR APPLICATION NUMBER: CA 2,305,036

PRIOR FILING DATE: 2000-04-12
PRIOR APPLICATION NUMBER: US 60/232,425
PRIOR FILING DATE: 2000-09-14
PRIOR APPLICATION NUMBER: CA 2,335,109
PRIOR FILING DATE: 2001-02-23
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 15
LENGTH: 31
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURES:
NAME/KEY: DOMAIN
LOCATION: (15)..(18)
OTHER INFORMATION: spacer monomers (such as the illustrated glycine
OTHER INFORMATION: G's) may be used in variable numbers, such as 2, 3
OTHER INFORMATION: Synthesised in Laboratory:
OTHER INFORMATION: SDF-1(1-14)-(G)4-SDF-1(55-67) amide: or CTCB0017
NAME/KEY: MOD RES
LOCATION: (31)
OTHER INFORMATION: AMIDATION
US-09-835-107-15

Query Match 93.8%; Score 158.5; DB 9; Length 31;
Best Local Similarity 96.8%; Pred. No. 1.4e-14;
Matches 30; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 KPVSLSYRCPCRFPGGGLKMIQIYLEYKALN 30
Db 1 KPVSLSYRCPCRFPGGGLKMIQIYLEYKALN 31

RESULT 7

US-09-835-107-20
Sequence 20, Application US/09835107
Patent No. US20020165123A1
GENERAL INFORMATION:
APPLICANT: Tudan, Christopher R.
APPLICANT: Merzouk, Ahmed
APPLICANT: Arab, Lakhdar
APPLICANT: Saxena, Geeta
APPLICANT: Bayes, Connie J.
APPLICANT: Cashman, Johanne
APPLICANT: Clark-Lewis
APPLICANT: Salari, Hassan
TITLE OF INVENTION: CXCR4 AGONIST TREATMENT OF HEMATOPOIETIC CELLS
FILE REFERENCE: SMAR012
CURRENT APPLICATION NUMBER: US/09/835,107
CURRENT FILING DATE: 2001-08-20
PRIOR APPLICATION NUMBER: CA 2,305,036
PRIOR FILING DATE: 2000-04-12
PRIOR APPLICATION NUMBER: US 60/232,425
PRIOR FILING DATE: 2000-09-14
PRIOR APPLICATION NUMBER: CA 2,335,109
PRIOR FILING DATE: 2001-02-23
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 20
LENGTH: 31
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURES:
NAME/KEY: DOMAIN
LOCATION: (15)..(18)
OTHER INFORMATION: spacer monomers (such as the illustrated glycine
OTHER INFORMATION: G's) may be used in variable numbers, such as 2, 3
OTHER INFORMATION: Synthesised in Laboratory:
OTHER INFORMATION: Cyclyzed, for example glutamate (E) and lysine (K)
OTHER INFORMATION: residues may be joined by side chain cyclization
OTHER INFORMATION: using a lactam formation procedure.

OTHER INFORMATION: Synthesised in laboratory;
OTHER INFORMATION: SDF-1(1-14)-(G)4-SDF(55-67)-B24/K28-cyclic acid
US-09-835-107-20

Query Match 93.8%; Score 158.5; DB 9; Length 31;
Best Local Similarity 96.8%; Pred. No. 1.4e-14;
Matches 30; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 KPVSLSYRCPCRF-GGGLKMIQIYLEKALN 30
Db 1 KPVSLSYRCPCRFGGGLKMIQIYLEKALN 31

RESULT 8

US-09-835-107-21
Sequence 21, Application US/09835107
Patent No. US20020165123A1
GENERAL INFORMATION:
APPLICANT: Tuden, Christopher R.
APPLICANT: Merzouk, Ahmed
APPLICANT: Arab, Lakhdar
APPLICANT: Saxena, Geeta
APPLICANT: Eaves, Connie J.
APPLICANT: Cashman, Johanne
APPLICANT: Clark-Lewis
APPLICANT: Salari, Hassan
TITLE OF INVENTION: CXCR4 AGONIST TREATMENT OF HEMATOPOIETIC CELLS
FILE REFERENCE: SWAR012
CURRENT APPLICATION NUMBER: US/09/835,107
CURRENT FILING DATE: 2001-08-20
PRIOR APPLICATION NUMBER: CA 2,305,036
PRIOR FILING DATE: 2000-04-12
PRIOR APPLICATION NUMBER: US 60/232,425
PRIOR FILING DATE: 2000-09-14
PRIOR APPLICATION NUMBER: CA 2,335,109
PRIOR FILING DATE: 2001-02-23
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 21
LENGTH: 31
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: DOMAIN
LOCATION: (15)..(18)
OTHER INFORMATION: spacer monomers (such as the illustrated glycine
OTHER INFORMATION: G's) may be used in variable numbers, such as 2, 3
OTHER INFORMATION: or 4 glycines.
NAME/KEY: DOMAIN
LOCATION: (20)..(24)
OTHER INFORMATION: Cyclized, for example glutamate (E) and lysine (K)
OTHER INFORMATION: residues may be joined by side chain cyclization
OTHER INFORMATION: using a laccam formation.
OTHER INFORMATION: Synthesised in laboratory;
OTHER INFORMATION: SDF-1(1-14)-(G)4-SDF(55-67)-K20/B24-cyclic acid
US-09-835-107-21

Query Match 93.8%; Score 158.5; DB 9; Length 31;
Best Local Similarity 96.8%; Pred. No. 1.4e-14;
Matches 30; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 KPVSLSYRCPCRF-GGGLKMIQIYLEKALN 30
Db 1 KPVSLSYRCPCRFGGGLKMIQIYLEKALN 31

RESULT 9

US-09-835-107-22
Sequence 22, Application US/09835107
Patent No. US20020165123A1
GENERAL INFORMATION:
APPLICANT: Tuden, Christopher R.
APPLICANT: Merzouk, Ahmed

APPLICANT: Arab, Lakhdar
APPLICANT: Saxena, Geeta
APPLICANT: Eaves, Connie J.
APPLICANT: Cashman, Johanne
APPLICANT: Clark-Lewis
APPLICANT: Salari, Hassan
TITLE OF INVENTION: CXCR4 AGONIST TREATMENT OF HEMATOPOIETIC CELLS
FILE REFERENCE: SWAR012
CURRENT APPLICATION NUMBER: US/09/835,107
CURRENT FILING DATE: 2001-08-20
PRIOR APPLICATION NUMBER: CA 2,305,036
PRIOR FILING DATE: 2000-04-12
PRIOR APPLICATION NUMBER: US 60/232,425
PRIOR FILING DATE: 2000-09-14
PRIOR APPLICATION NUMBER: CA 2,335,109
PRIOR FILING DATE: 2001-02-23
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 22
LENGTH: 31
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: DOMAIN
LOCATION: (15)..(18)
OTHER INFORMATION: spacer monomers (such as the illustrated glycine
OTHER INFORMATION: G's) may be used in variable numbers, such as 2, 3
OTHER INFORMATION: or 4 glycines.
NAME/KEY: DOMAIN
LOCATION: (24)..(28)
OTHER INFORMATION: Cyclized, for example (E) and lysine (K) residues
OTHER INFORMATION: may be joined by side chain cyclization using a
OTHER INFORMATION: laccam formation procedure.
OTHER INFORMATION: Synthesised in laboratory;
OTHER INFORMATION: SDF-1(1-14)-(G)4-SDF(55-67)-B24/K28-cyclic
OTHER INFORMATION: amide; or CTC80022
NAME/KEY: MOD RES
LOCATION: (31)
OTHER INFORMATION: AMIDATION
US-09-835-107-22

Query Match 93.8%; Score 158.5; DB 9; Length 31;
Best Local Similarity 96.8%; Pred. No. 1.4e-14;
Matches 30; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 KPVSLSYRCPCRF-GGGLKMIQIYLEKALN 30
Db 1 KPVSLSYRCPCRFGGGLKMIQIYLEKALN 31

RESULT 10

US-09-835-107-23
Sequence 23, Application US/09835107
Patent No. US20020165123A1
GENERAL INFORMATION:
APPLICANT: Tuden, Christopher R.
APPLICANT: Merzouk, Ahmed
APPLICANT: Arab, Lakhdar
APPLICANT: Saxena, Geeta
APPLICANT: Eaves, Connie J.
APPLICANT: Cashman, Johanne
APPLICANT: Clark-Lewis
APPLICANT: Salari, Hassan
TITLE OF INVENTION: CXCR4 AGONIST TREATMENT OF HEMATOPOIETIC CELLS
FILE REFERENCE: SWAR012
CURRENT APPLICATION NUMBER: US/09/835,107
CURRENT FILING DATE: 2001-08-20
PRIOR APPLICATION NUMBER: CA 2,305,036
PRIOR FILING DATE: 2000-04-12
PRIOR APPLICATION NUMBER: US 60/232,425
PRIOR FILING DATE: 2000-09-14
PRIOR APPLICATION NUMBER: CA 2,335,109
PRIOR FILING DATE: 2001-02-23

NUMBER OF SEQ ID NOS: 34
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 23
LENGTH: 31
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: DOMAIN
LOCATION: (15)..(18)
OTHER INFORMATION: spacer monomers (such as the illustrated glycine
OTHER INFORMATION: G's) may be used in variable numbers, such as 2, 3
OTHER INFORMATION: or 4 glycines.
NAME/KEY: DOMAIN
LOCATION: (20)..(24)
OTHER INFORMATION: cyclized, for example glutamate (E) and lysine
OTHER INFORMATION: (K) residues may be joined by side chain
OTHER INFORMATION: cyclization using a lactam formation procedure.
OTHER INFORMATION: Synthesised in Laboratory:
OTHER INFORMATION: SDF-1(1-14)-(G)4-SDF-1(55-67)-K20/E24-cyclic
NAME/KEY: MOD_RES
LOCATION: (31)
OTHER INFORMATION: amide: or CTCB0021
US-09-835-107-23

Query Match 93.8%; Score 158.5; DB 9; Length 31;
Best Local Similarity 96.8%; Pred. No. 1.4e-14;
Matches 30; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 KPVSLSYRCPCRFP-GGGLKMIQIYLEKALN 30
Db 1 KPVSLSYRCPCRFPGGGLKMIQIYLEKALN 31

RESULT 11
US-09-835-107-26
Sequence 26, Application US/09835107
Patent No. US20020165123A1
GENERAL INFORMATION:
APPLICANT: Tudan, Christopher R.
APPLICANT: Merzouk, Ahmed
APPLICANT: Arab, Lakhdar
APPLICANT: Saxena, Geeta
APPLICANT: Eaves, Connie J.
APPLICANT: Cashman, Johanne
APPLICANT: Clark-Lewis
APPLICANT: Salari, Hassan
TITLE OF INVENTION: CXCR4 AGONIST TREATMENT OF HEMATOPOIETIC CELLS
FILE REFERENCE: SMAR012
CURRENT APPLICATION NUMBER: US/09/835,107
PRIOR FILING DATE: 2001-08-20
PRIOR APPLICATION NUMBER: CA 2,305,036
PRIOR FILING DATE: 2000-04-12
PRIOR APPLICATION NUMBER: US 60/232,425
PRIOR FILING DATE: 2000-09-14
PRIOR APPLICATION NUMBER: CA 2,335,109
PRIOR FILING DATE: 2001-02-23
NUMBER OF SEQ ID NOS: 34
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 26
LENGTH: 31
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: DOMAIN
LOCATION: (15)..(18)
OTHER INFORMATION: spacer monomers (such as the illustrated glycine
OTHER INFORMATION: G's) may be used in variable numbers, such as 2, 3
OTHER INFORMATION: or 4 glycines.
NAME/KEY: DISULFID
LOCATION: (9)..(11)
OTHER INFORMATION: cysteine residues may for example be involved in
OTHER INFORMATION: bridge formation

OTHER INFORMATION: Synthesised in Laboratory:
OTHER INFORMATION: SDF-1(1-14)-(G)4-SDF-1(55-67)-C9/C11-cyclic acid
US-09-835-107-26

Query Match 93.8%; Score 158.5; DB 9; Length 31;
Best Local Similarity 96.8%; Pred. No. 1.4e-14;
Matches 30; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 KPVSLSYRCPCRFP-GGGLKMIQIYLEKALN 30
Db 1 KPVSLSYRCPCRFPGGGLKMIQIYLEKALN 31

RESULT 12
US-09-835-107-27
Sequence 27, Application US/09835107
Patent No. US20020165123A1
GENERAL INFORMATION:
APPLICANT: Tudan, Christopher R.
APPLICANT: Merzouk, Ahmed
APPLICANT: Arab, Lakhdar
APPLICANT: Saxena, Geeta
APPLICANT: Eaves, Connie J.
APPLICANT: Cashman, Johanne
APPLICANT: Clark-Lewis
APPLICANT: Salari, Hassan
TITLE OF INVENTION: CXCR4 AGONIST TREATMENT OF HEMATOPOIETIC CELLS
FILE REFERENCE: SMAR012
CURRENT APPLICATION NUMBER: US/09/835,107
PRIOR FILING DATE: 2001-08-20
PRIOR APPLICATION NUMBER: CA 2,305,036
PRIOR FILING DATE: 2000-04-12
PRIOR APPLICATION NUMBER: US 60/232,425
PRIOR FILING DATE: 2000-09-14
PRIOR APPLICATION NUMBER: CA 2,335,109
PRIOR FILING DATE: 2001-02-23
NUMBER OF SEQ ID NOS: 34
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 27
LENGTH: 31
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: DOMAIN
LOCATION: (15)..(18)
OTHER INFORMATION: spacer monomers (such as the illustrated glycine
OTHER INFORMATION: G's) may be used in variable numbers, such as 2, 3
OTHER INFORMATION: or 4 glycines.
NAME/KEY: DISULFID
LOCATION: (9)..(11)
OTHER INFORMATION: Cysteine residues may for example be involved in
OTHER INFORMATION: bridge formation.
OTHER INFORMATION: Synthesised in Laboratory:
OTHER INFORMATION: SDF-1(1-14)-(G)4-SDF-1(55-67)-C9/C11-cyclic amide
NAME/KEY: MOD_RES
LOCATION: (31)
OTHER INFORMATION: AMIDATION
US-09-835-107-27

Query Match 93.8%; Score 158.5; DB 9; Length 31;
Best Local Similarity 96.8%; Pred. No. 1.4e-14;
Matches 30; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 KPVSLSYRCPCRFP-GGGLKMIQIYLEKALN 30
Db 1 KPVSLSYRCPCRFPGGGLKMIQIYLEKALN 31

RESULT 13
US-10-086-177A-13
Sequence 13, Application US/10086177A
Publication No. US20030148940A1
GENERAL INFORMATION:

```
APPLICANT: Tudan, Christopher R.
APPLICANT: Merzouk, Ahmed
APPLICANT: Saxena, Geeta
APPLICANT: Baves, Connie J.
APPLICANT: Cashman, Johanne
APPLICANT: Clark-Lewis, Ian
APPLICANT: Salari, Hassan
TITLE OF INVENTION: CXCR Agonist Treatment of Hematopoietic
FILE REFERENCE: SMAR-012CIP
CURRENT APPLICATION NUMBER: US/10/086,177A
CURRENT FILING DATE: 2002-02-26
PRIOR APPLICATION NUMBER: 09/835,107
PRIOR FILING DATE: 2001-04-12
PRIOR APPLICATION NUMBER: 60/232,425
PRIOR FILING DATE: 2000-09-14
PRIOR APPLICATION NUMBER: CA 2,305,036
PRIOR FILING DATE: 2000-04-12
PRIOR APPLICATION NUMBER: CA 2,335,109
PRIOR FILING DATE: 2001-02-23
NUMBER OF SEQ ID NOS: 34
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 13
LENGTH: 31
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthesized in Laboratory: SDF-1 (1-14) - (G)
US-10-086-177A-13
```

```
Query Match          93.8%; Score 158.5; DB 14; Length 31;
Best Local Similarity 96.8%; Pred. No. 1.4e-14;
Matches 30; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
```

```
OY      1 KPVSLSTRCPGRPF-GGGGLKMIQIYLEKALN 30
Db      1 KPVSLSTRCPGRPFGGGLKMIQIYLEKALN 31
```

```
RESULT 14
US-10-086-177A-15
Sequence 15, Application US/10086177A
Publication No. US20030148940A1
GENERAL INFORMATION:
APPLICANT: Tudan, Christopher R.
APPLICANT: Merzouk, Ahmed
APPLICANT: Saxena, Geeta
APPLICANT: Baves, Connie J.
APPLICANT: Cashman, Johanne
APPLICANT: Clark-Lewis, Ian
APPLICANT: Salari, Hassan
TITLE OF INVENTION: CXCR Agonist Treatment of Hematopoietic
FILE REFERENCE: SMAR-012CIP
CURRENT APPLICATION NUMBER: US/10/086,177A
CURRENT FILING DATE: 2002-02-26
PRIOR APPLICATION NUMBER: 09/835,107
PRIOR FILING DATE: 2001-04-12
PRIOR APPLICATION NUMBER: 60/232,425
PRIOR FILING DATE: 2000-09-14
PRIOR APPLICATION NUMBER: CA 2,305,036
PRIOR FILING DATE: 2000-04-12
PRIOR APPLICATION NUMBER: CA 2,335,109
PRIOR FILING DATE: 2001-02-23
NUMBER OF SEQ ID NOS: 34
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 15
LENGTH: 31
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthesized in Laboratory: SDF-1 (1-14) - (G)
```

```
OTHER INFORMATION: 3-SDF-1 (55-67) amide: or CTCB0017
US-10-086-177A-15
```

```
Query Match          93.8%; Score 158.5; DB 14; Length 31;
Best Local Similarity 96.8%; Pred. No. 1.4e-14;
Matches 30; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
```

```
OY      1 KPVSLSTRCPGRPF-GGGGLKMIQIYLEKALN 30
Db      1 KPVSLSTRCPGRPFGGGLKMIQIYLEKALN 31
```

```
RESULT 15
US-10-086-177A-20
Sequence 20, Application US/10086177A
Publication No. US20030148940A1
GENERAL INFORMATION:
APPLICANT: Tudan, Christopher R.
APPLICANT: Merzouk, Ahmed
APPLICANT: Saxena, Geeta
APPLICANT: Baves, Connie J.
APPLICANT: Cashman, Johanne
APPLICANT: Clark-Lewis, Ian
APPLICANT: Salari, Hassan
TITLE OF INVENTION: CXCR Agonist Treatment of Hematopoietic
FILE REFERENCE: SMAR-012CIP
CURRENT APPLICATION NUMBER: US/10/086,177A
CURRENT FILING DATE: 2002-02-26
PRIOR APPLICATION NUMBER: 09/835,107
PRIOR FILING DATE: 2001-04-12
PRIOR APPLICATION NUMBER: 60/232,425
PRIOR FILING DATE: 2000-09-14
PRIOR APPLICATION NUMBER: CA 2,305,036
PRIOR FILING DATE: 2000-04-12
PRIOR APPLICATION NUMBER: CA 2,335,109
PRIOR FILING DATE: 2001-02-23
NUMBER OF SEQ ID NOS: 34
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 20
LENGTH: 31
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthesized in Laboratory: SDF-1 (1-14) - (G)
US-10-086-177A-20
```

```
Query Match          93.8%; Score 158.5; DB 14; Length 31;
Best Local Similarity 96.8%; Pred. No. 1.4e-14;
Matches 30; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
```

```
OY      1 KPVSLSTRCPGRPF-GGGGLKMIQIYLEKALN 30
Db      1 KPVSLSTRCPGRPFGGGLKMIQIYLEKALN 31
```

```
Search completed: January 4, 2005, 16:04:59
Job time : 97.8689 secs
```

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 4, 2005, 15:43:59 ; Search time 12.2951 Seconds
(without alignments)
234.769 Million cell updates/sec

Title: US-10-086-177A-12

Perfect score: 169
Sequence: 1 KPVSLSYRCPCRFPGGSLKWIQYLEKALN 30

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: PIR.79:*
2: p1r1:*
3: p1r2:*
4: p1r3:*
5: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	118.5	70.1	89	2	IS3416 interluekin-8 homo
2	118.5	70.1	89	2	AS3497 pre-B-cell growth-
3	118.5	70.1	93	2	G01540 cytokine SDF-1-beta
4	118.5	70.1	93	2	I81182 cytokine - mouse
5	59.5	35.2	1084	2	T08583 cellulose synthase
6	59.5	35.2	1088	2	H84604 probable cellulose
7	56.5	33.4	1081	2	T52028 cellulose synthase
8	54.5	32.2	233	2	T35594 hypothetical prote
9	54.5	32.2	1400	2	T22644 cellulose synthase
10	52	30.8	974	2	T10797 genome polyprotein
11	50.5	29.9	3433	1	GNMVKV DNA-directed RNA p
12	49.5	29.3	189	2	DS9389 probable class III
13	49.5	29.3	469	2	CS3345 tryptophan 2-monoo
14	49.5	29.3	556	1	AS3376 catechol oxidase f
15	49.5	29.3	557	1	AS2493 ADP-ribosylation f
16	49.5	29.3	588	2	S34786 probable RNA-bind
17	49.5	29.3	1147	2	T42627 probable RNA-bind
18	49	29.0	347	2	T51547 hypothetical prote
19	49	29.0	347	2	I51546 hypothetical prote
20	49	29.0	439	2	E72288 Ig heavy chain - n
21	49	29.0	577	2	I50731 cellulose synthase
22	48.5	28.7	685	2	T10800 homeotic protein 1
23	48.5	28.7	1429	2	S06434 hypothetical prote
24	48	28.4	312	2	T23493 hypothetical prote
25	48	28.4	340	2	T33492 hypothetical prote
26	47.5	28.1	212	2	S73466 probable alpha-1,2
27	47.5	28.1	378	2	T11713 probable RNA polym
28	47	27.8	311	2	H71252 acetate kinase ack
29	47	27.8	390	2	S73635

30	47	27.8	402	2	T14438 phosphate/triose-p
31	47	27.8	618	2	T00476 probable vacuolar
32	47	27.8	805	2	A69682 primosomal replica
33	47	27.8	1008	2	T30544 major surface glyco
34	46.5	27.5	431	2	T29716 gamma-aminobutyrate
35	46.5	27.5	470	2	T46814 diaminobutyrate-py
36	46.5	27.5	470	2	B95419 probable phenylala
37	46.5	27.5	548	2	E72457 succinate dehydrog
38	46	27.2	122	2	T45165 hypothetical prote
39	46	27.2	161	2	B84366 hypothetical prote
40	46	27.2	247	2	T02393 hypothetical prote
41	46	27.2	262	2	B95289 hypothetical prote
42	46	27.2	379	2	T06610 hypothetical prote
43	46	27.2	393	2	E64239 acetate kinase (BC
44	46	27.2	804	2	E83963 primosomal replica
45	46	27.2	1017	2	T08553 hypothetical prote

ALIGNMENTS

RESULT 1

153416 interluekin-8 homolog - mouse
C:Species: Mus sp. (mouse)
C>Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 05-Nov-1999
C/Accession: 153416
R/Jiang, W.; Zhou, P.; Kahn, S.M.; Tomita, N.; Johnson, M.D.; Weinstein, I.B.
Exp. Cell Res. 215, 284-293, 1994
A/Title: Molecular cloning of TPRL, a gene whose expression is repressed by the tumor
A/Reference number: 153416; MUID:95073497; PMID:7982471
A/Accession: 153416
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-89 <RES>
A/Cross-references: GB:574318; NID:9786393; PIDN:AA832650.1; PID:9786394
C/Genetics:
A/Gene: TPRL
C/Superfamily: beta-thromboglobulin

Query Match 70.1%; Score 118.5; DB 2; Length 89;
Best Local Similarity 40.3%; Pred. No. 3.5e-09;
Matches 27; Conservative 0; Mismatches 3; Indels 37; Gaps 1;

Qy	1	KPVSLSYRCPCRFPGG-----GLKWIQ 23
Db	22	KPVSLSYRCPCRFPGGSLKWIQYLEK 81
Qy	24	YLEKALN 30
Db	82	YLEKALN 88

RESULT 2

AS3497 pre-B-cell growth-stimulating factor precursor - mouse
C/Species: Mus musculus (house mouse)
C/Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 09-Jul-2004
C/Accession: AS3497; I59582
R/Nagasaki, T.; Kikutani, H.; Kishimoto, T.
Proc. Natl. Acad. Sci. U.S.A. 91, 2305-2309, 1994
A/Title: Molecular cloning and structure of a pre-B-cell growth-stimulating factor.
A/Reference number: AS3497; MUID:94181581; PMID:8134392
A/Accession: AS3497
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-89 <NMG>
A/Cross-references: UNIPROT:P40224; GB:D21072; NID:g413905; PIDN:BA04648.1; PID:g46845
R/Ishino, K.; Tada, H.; Heikner, R.; Shirozu, M.; Nakano, T.; Honjo, T.
Science 261, 600-603, 1993
A/Title: Signal sequence trap: a cloning strategy for secreted proteins and type I memb
A/Reference number: I59582; MUID:93342488; PMID:8342023
A/Accession: I59582

A:Stratuc: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-89 <RES>
A:Cross-references: GB:U12029, NID:G393179, PIDN:AAA40100.1, PID:G393180
A:Genetics:
A:Gene: SDF-1- α pha
C:Superfamily: beta-chromoglobulin
C:Keywords: cytokine

Query Match	70.1%;	Score 118.5;	DB 2;	length 89;
Best Local Similarity	40.3%;	Pred. No. 3.5e-09;		
Matches	27;	Conservative	0;	Mismatches 3;
			Indels	37;
			Gaps	1;

```

RESULT 3
G01540
cytokine SDF-1-beta - human
C:Species: Homo sapiens (man)
C:Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #ext_change 09-Jul-2004
C:Accession: G01540
R:Spotila, L.D.
submitted to the EMBL Data Library, October 1994
A:Reference number: G07697
A:Accession: G01540
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-93 <SPO>
A:Cross-references: UNIPROT:P48061; EMBL:U16752;
C:Superfamily: beta-chromodomain
C:Superfamily: beta-chromodomain

```

Query Match	70.1%;	Score 118.5;	DB 2;	Length 93;
Best Local Similarity	40.3%;	Pred. No. 3.6e-09;		
Matches 27;	Conservative 0;	Mismatches 3;	Indels 37;	Gaps 1;

RESULT 4
 18182
 cytokine - mouse
 C.Species: Mus musculus (house mouse)
 C.Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 09-Jul-2004
 C.Accession: I81182
 R.Tsahiro, K.; Tada, H.; Hellker, R.; Shirozu, M.; Nakano, T.; Honjo, T.
 Science 261, 600-603, 1993
 A>Title: Signal sequence trap: a cloning strategy for secreted proteins and type I membn
 A.Reference number: 159582; MUID:93342488; PMID:3342023
 A.Accession: I81182
 A.Status: preliminary; translated from GB/EMBL/DBJ
 A.Molecule type: mRNA
 A.Residues: 1-93 <RES>
 A.Cross-references: UNIPROT:P40224; GB:LI2030; NID:G393181; PIDN:AAA40101.1; PID:G393182
 C.Genetics:
 A:Gene: SDF-1-beta
 C:Superfamily: Beta-chromoglobulin

Query Match	70.1%;	Score 118.5;	DB 2;	Length 93;
Best Local Similarity	40.3%;	Pred. No. 3.6e-09;		
Matches 27; Conservative	0;	Mismatches 3;	Indels 37;	Gaps 14;

```
Qy 1 KPVSLSPRCRCRFFGG-----GLKMIQ 23
    |||||
Db 22 KPVSLSPRCRCRFFESHIAANVNHKLINTPNCALQIVARLKNRRNQYCIDPKLMIQE 81
    |||||
Qy 24 YLEKALN 30
    |||||
Db 82 YLEKALN 88
```

RESULT 5
T08583
cellulose synthase (EC 2.4.1.-) catalytic chain - Arabidopsis thaliana
N|Alternate names: protein T22P8.250
C|Species: Arabidopsis thaliana (mouse-ear cress)
C|Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C|Accession: T08583; T08014
R|Beyran, M.; Zimmermann, W.; Gruenleisen, A.; Mambut, R.; Bancroft, I.; Mewes, H.-W.; May, submitted to the Protein Sequence Database, May 1999
A|Reference number: Z16442

A: Molecule type: DNA
A: Residues: 1-1084 <BEV>
A: Cross-references: UNIPROT:O48947; EMBL:AL050351; GSPDB:GN00062; ATSP:T22F8.250
A: Experimental source: CULTIVAR Columbia; BAC clone T72F8
R: Artoli, T.; Peng, L.; Betner, A.S.; Burn, J.; Wiltke, W.; Herth, W.; Camilleri, C.; ;
Science 279, 717-720, 1998
A: Title: Molecular analysis of cellulose biosynthesis in Arabidopsis.
A: Reference number: Z13745; MUID:9811412; PMID:9445479
A: Accession: T09014
A: Status: translated from GB/EMBL/DDBB
A: Molecule type: mRNA
A: Residues: 1-1084 <R1>
A: Cross-references: EMBL:AF027173; NID:G2827140; PIDN:AAC9335.1; PID:G2827141
A: Experimental source: cultivar Columbia
C: Genetics:
A: Gene: ATSP:T22F8.250; Ath-A
A: Map position: 4
A: Introns: 27/3; 156/3; 191/1; 254/2; 343/2; 458/3; 504/3; 546/3; 617/3; 708/1; 773/3;
A: Keywords: cell wall synthesis; glycosyltransferase; hexosyltransferase

Query Match	35.2%	Score 59.5	DB 2	Length 1084
Best Local Similarly	43.5%	Pred. No. 4.1		
Matches 10	Conservative 6	Mismatches 6	Indels 1	Gaps 1

RESULT 6
 H84604
 Probable cellulose synthase catalytic subunit [imported] - Arabidopsis thaliana
 C/Species: Arabidopsis thaliana (mouse-ear cress)
 C/Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
 C/Accession: H84604
 R/Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Bentol, M.I.; Town, C.D.; Fujii, C.Y.;
 M.; Koo, H.; Moffatt, K.S.; Cronin, L.A.; Shen, M.; Vanden, S.B.; Umayam, L.; Tallon, L.
 euse, D.; Nieman, C.S.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter,
 Nature 402, 761-768, 1999
 A/TITLE: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
 A/Reference number: AB84420; MUID:20083487; PMID:10617197

```
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1088 <STO>
A:Cross-references: UNIPROT:Q9S2J2; GB:AE002093; NID:94417271; PIDN:AAD20396.1; GSPDB:GT
C:Genetics:
A:Gene: A12g21770
A:Map position: 2
```

Query Match	35.2%	Score 59.5;	DB 2;	Length 1088;
Best Local Similarity	43.5%	Pred. No. 4.1;		

Matches 10; Conservative 6; Mismatches 6; Indels 1; Gaps 1;

QY 3 VSLSYRCPCRF-FGGGLKMIQ 24

Db 837 IFLSRHCPIMWYGGLKMLERF 859

RESULT 7

T52028 cellulose synthase [imported] - Arabidopsis thaliana (fragment)

C/Species: Arabidopsis thaliana (mouse-ear cress)

C/Date: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 09-Jul-2004

C/Accession: T52028

R/Joshi, C.

submitted to the EMBL Data Library, May 1998

A/Reference number: Z25890

A/Accession: T52028

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-1081 <OIS>

A/Cross-references: UNIPROT:O65338; EMBL:AF062485; PIDN:AA029067.1

Query Match

33.4%; Score 56.5; DB 2; Length 1081;

Best Local Similarity 47.6%; Pred. No. 11;

Matches 10; Conservative 5; Mismatches 5; Indels 1; Gaps 1;

QY 3 VSLSYRCPCRF-FGGGLKMIQ 22

Db 831 IFLSRHCPIMWYGGLKMLE 851

RESULT 8

T35594

hypothetical protein SC6G4.43c SC6G4.43c - Streptomyces coelicolor

C/Species: Streptomyces coelicolor

C/Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 09-Jul-2004

C/Accession: T35594

R/Saunders, D.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.

submitted to the EMBL Data Library, August 1998

A/Reference number: Z21583

A/Accession: T35594

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-233 <SAU>

A/Cross-references: UNIPROT:O86804; EMBL:AL031317; PIDN:CAA20421.1; GSPDB:GN00070; SCOP

A/Experimental source: strain A3(2)

C/Genetics:

A/Gene: SC6G4.43c

C/Superfamily: hypothetical protein HI0278

Query Match

32.2%; Score 54.5; DB 2; Length 233;

Best Local Similarity 40.0%; Pred. No. 5.1;

Matches 10; Conservative 6; Mismatches 6; Indels 3; Gaps 1;

QY 6 SYRCPCRFPGGL---KMIQVLEK 27

Db 135 SGRIPCRFQGHGMBPRWVKRPMK 159

RESULT 9

T22644

hypothetical protein F54D1.5 - Caenorhabditis elegans

C/Species: Caenorhabditis elegans

C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C/Accession: T22644

R/Lennard, N.

submitted to the EMBL Data Library, July 1996

A/Reference number: Z19592

A/Accession: T22644

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-1400 <WTL>

A/Cross-references: UNIPROT:Q20766; EMBL:Z77132; PIDN:CAB00861.1; GSPDB:GN00022; CESP:FS

A/Experimental source: clone F54D1

C/Genetics:

A/Gene: CESP:F54D1.5

A/Map position: 4

A/Intons: 21/2; 51/2; 205/2; 276/3; 364/2; 394/2; 466/3; 507/3; 536/3; 599/3; 672/2; 6

Query Match

32.2%; Score 54.5; DB 2; Length 1400;

Best Local Similarity 42.9%; Pred. No. 25;

Matches 12; Conservative 3; Mismatches 10; Indels 3; Gaps 1;

QY 3 VSLSYRCPCRFPGGLKMIQVLEKALN 30

Db 476 VDLAKSC---LFGNGRMSSDVLEKMN 500

RESULT 10

T10797

cellulose synthase (EC 2.4.1.-) catalytic chain celA1 - upland cotton

C/Species: Gossypium hirsutum (upland cotton)

C/Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004

C/Accession: T10797

R/Pear, J.R.; Kawagoe, Y.; Schreckengost, W.E.; Delmer, D.P.; Stalker, D.M.

Proc. Natl. Acad. Sci. U.S.A. 93, 12637-12642, 1996

A/Title: Higher plants contain homologs of the bacterial celA genes encoding the cataly

A/Reference number: Z17152; MUID:97057296; PMID:8901635

A/Accession: T10797

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-974 <PEA>

A/Cross-references: UNIPROT:P91155; EMBL:U58283; NID:g1706955; PIDN:AAB37766.1; PID:g17

A/Experimental source: strain Acala S2-2; fiber

C/Genetics:

A/Gene: celA1

C/Function:

A/Description: involved in the synthesis of cellulose

C/Keywords: glycosyltransferase; hexosyltransferase

Query Match

30.8%; Score 52; DB 2; Length 974;

Best Local Similarity 54.5%; Pred. No. 40;

Matches 12; Conservative 3; Mismatches 5; Indels 2; Gaps 2;

QY 3 VSLSYRCPCRF-FGGGLKMIQ 22

Db 721 IFLSRHCPIMWYGGLKMLQ 742

RESULT 11

GNMYKV

genome polyprotein - Kunjin virus (strain MRM61C)

N/Contains: capsid protein C; envelope protein E; membrane protein M; nonstructural pro

in NS4a; nonstructural protein NS4b; nonstructural protein NS5

C/Species: Kunjin virus

C/Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 09-Jul-2004

C/Accession: A28697

R/Cola, G.; Parker, M.D.; Speight, G.; Byrne, M.E.; Westaway, E.G.

J. Gen. Virol. 69, 1-21, 1988

A/Title: Nucleotide and complete amino acid sequences of Kunjin virus: definitive gene

A/Reference number: A28697; MUID:88089524; PMID:2826559

A/Accession: A28697

A/Molecule type: genomic RNA

A/Residues: 1-3433 <COI>

A/Cross-references: UNIPROT:P14335; GB:D00246; NID:g221966; PIDN:BAA00176.1; PID:g22196

C/Superfamily: yellow fever virus genome polyprotein

C/Keywords: ATP; capsid protein; envelope protein; membrane protein; nonstructural prot

F/2-123/Product: capsid protein C #status predicted <CPC>

F/124-290/Product: membrane protein M precursor #status predicted <MPP>

F/124-215/Domain: nonterminal signal sequence #status predicted <SIG>

F/216-280/Product: membrane protein M #status predicted <MPM>

F/291-791/Product: envelope protein E #status predicted <EP>

F/792-1143/Product: nonstructural protein NS1 #status predicted <NS1>

F/1144-1374/Product: nonstructural protein NS2a #status predicted <NS2a>

F/1375-1505/Product: nonstructural protein NS2b #status predicted <NS2b>

F/1506-2124/Product: nonstructural protein NS3 #status predicted <NS3>

F:1699-1706/Region: nucleotide-binding motif A (P-loop)
F:1786-1793/Region: nucleotide-binding motif B

F:1790-1793/Region: DBA motif
F:2125-2273/Product: nonstructural protein NS4a #status predicted <NA>
F:2274-2528/Product: nonstructural protein NS4b #status predicted <NA>
F:2529-3433/Product: nonstructural protein NS5 #status predicted <NS5>

Query Match 29.9% Score 50.5; DB 1; Length 3433;
Best Local Similarity 37.9%; Pred. No. 2e+02;
Matches 11; Conservative 5; Mismatches 12; Indels 1; Gaps 1;

QY 2 PVSLSYRCPCRFPGGGLKWIQVLEKAL 29
DB 1837 PISDLQTEIPDRAWNSGVEMTEYIGKTV 1865

RESULT 12

DNA-directed RNA polymerase, subunit E' (rpoB1) homolog - Archaeoglobus fulgidus
C/Species: Archaeoglobus fulgidus
C/Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004

C/Accession: D69389
R/Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson
J.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.;
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997

A/Authors: Uteerback, T.; Cotton, M.D.; Spriggs, T.; Artlich, P.; Kaine, B.P.; Sykes, S.
Smith, H.O.; Woese, C.R.; Venter, J.C.
A/Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaea
A/Reference number: A69450; MUID:98049343; PMID:9389475
A/Accession: D69389

A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-189 <KLE>

A/Cross-references: UNIPROT:O29148; GB:AE001027; GB:AE000782; NID:G2689350; PTDN:AA89012
C/Superfamily: DNA-directed RNA polymerase subunit E

Query Match 29.3% Score 49.5; DB 2; Length 189;
Best Local Similarity 40.7%; Pred. No. 21;

Matches 11; Conservative 6; Mismatches 7; Indels 3; Gaps 1;

QY 3 VSLSYRCPCRFPGGGLKWIQVLEKAL 29
DB 161 IGLTRQP---WLGALKWIEEIKLM 184

RESULT 13

C83345
probable class III aminotransferase PA2413 [imported] - Pseudomonas aeruginosa (strain F
C/Species: Pseudomonas aeruginosa
C/Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004

C/Accession: C83345
R/Schover, C.K.; Pham, X.Q.; Eryin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; B
adman, S.; Yun, Y.; Brody, L.V.; Coulter, S.N.; Folger, K.R.; Kaas, A.; Lardig, K.; Lim,
J.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000

A/Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
A/Reference number: A82950; MUID:20437337; PMID:10984043
A/Accession: C83345

A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-469 <STO>

A/Cross-references: UNIPROT:Q91168; GB:AE004668; GB:AE004091; NID:G9948446; PTDN:AA0586
C/Experimental source: strain PA01
A/Genetic: PA2413

Query Match 29.3% Score 49.5; DB 2; Length 469;
Best Local Similarity 43.3%; Pred. No. 46;

Matches 13; Conservative 1; Mismatches 15; Indels 1; Gaps 1;

QY 2 PVSLSYRCPCRFPGGGLKWIQVLEKAL 30
DB 1837 PISDLQTEIPDRAWNSGVEMTEYIGKTV 1865

DB 199 PYPDYRCPEGLGEGAVKANLHYENLNLN 228

RESULT 14

A53376
tryptophan 2-monooxygenase (EC 1.13.12.3) - Pseudomonas syringae pv. syringae
C/Species: Pseudomonas syringae pv. syringae
C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004

C/Accession: A53376
R/Mazzola, M.; White, F.F.
J. Bacteriol. 176, 1374-1382, 1994

A/Title: A mutation in the indole-3-acetic acid biosynthesis pathway of Pseudomonas syri
A/Reference number: A53376; MUID:94156842; PMID:8113177

A/Accession: A53376
A/Status: preliminary

A/Molecule type: DNA
A/Residues: 1-556 <MAZ>

A/Cross-references: UNIPROT:Q52367; GB:U04358; NID:G472559; PTDN:AAA17678.1; PID:G47256

A/Genetic: laam
C/Superfamily: Pseudomonas tryptophan 2-monooxygenase

Query Match 29.3% Score 49.5; DB 1; Length 556;
Best Local Similarity 45.5%; Pred. No. 53;
Matches 10; Conservative 3; Mismatches 6; Indels 3; Gaps 1;

QY 9 CPCRFGGGLKWIQVLEKALN 30
DB 510 CSCSPFAGG---WIEGAVQTALN 528

RESULT 15

A25493
tryptophan 2-monooxygenase (EC 1.13.12.3) - Pseudomonas syringae pv. savastanoi
C/Species: Pseudomonas syringae pv. savastanoi
C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004

C/Accession: A25493
R/Yamada, T.; Palm, C.J.; Brooks, B.; Kogure, T.
Proc. Natl. Acad. Sci. U.S.A. 82, 6522-6526, 1985

A/Title: Nucleotide sequences of the Pseudomonas savastanoi indoleacetic acid genes sho
A/Reference number: A94062
A/Molecule type: DNA

A/Residues: 1-557 <YAM>

A/Cross-references: UNIPROT:P06617

A/Genetic: laam

C/Superfamily: Pseudomonas tryptophan 2-monooxygenase

C/Keywords: monooxygenase; oxidoreductase

Query Match 29.3% Score 49.5; DB 1; Length 557;
Best Local Similarity 45.5%; Pred. No. 54;
Matches 10; Conservative 3; Mismatches 6; Indels 3; Gaps 1;

QY 9 CPCRFGGGLKWIQVLEKALN 30
DB 511 CSCSPFAGG---WIEGAVQTALN 529

Search completed: January 4, 2005, 15:44:32
Job time: 13.2951 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 4, 2005, 15:43:59 ; Search time 57.541 Seconds

(without alignments)
299,982 Million cell updates/sec

Title: US-10-086-177A-12

Perfect score: 169
Sequence: 1 KPVSLSYRCPCRFPGSLKWIQYLEKALN 30

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : UniProt 02:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	118.5	70.1	89	1 SDF1_MOUSE	P40224 mus musculus
2	118.5	70.1	89	2 Q8HYF0	Q8HYF0 macaca mulatta
3	118.5	70.1	89	2 BA28601	BA28601 felis sil
4	118.5	70.1	89	2 CAC10203	CAC10203 homo sapi
5	118.5	70.1	89	2 BAC32216	BAC32216 mus muscu
6	118.5	70.1	89	2 BAC35845	BAC35845 mus muscu
7	118.5	70.1	89	2 CAG29279	CAG29279 homo sapi
8	118.5	70.1	92	2 Q9H554	Q9H554 homo sapien
9	118.5	70.1	93	1 SDF1_FELCA	SDF1_FELCA felis silve
10	118.5	70.1	93	1 SDF1_HUMAN	SDF1_HUMAN homo sapien
11	118.5	70.1	116	2 Q6EKW4	Q6EKW4 sus scrofa
12	118.5	70.1	137	2 Q80ZM4	Q80ZM4 mus musculus
13	117.5	69.5	89	2 Q6T7C0	Q6T7C0 gallus galli
14	117.5	69.5	89	2 AAR88102	AAR88102 gallus galli
15	117.5	69.5	89	2 AAR91695	AAR91695 gallus galli
16	117.5	69.5	131	2 Q6T7B9	Q6T7B9 gallus galli
17	117.5	69.5	131	2 AAR91696	AAR91696 gallus galli
18	115.5	68.3	89	2 Q9OZD1	Q9OZD1 rattus norv
19	115.5	68.3	119	2 Q80YV8	Q80YV8 rattus norv
20	108.5	64.2	94	2 Q8UUV9	Q8UUV9 xenopus lae
21	108.5	64.2	94	2 AAH61945	AAH61945 xenopus lae
22	59.5	35.2	507	2 Q93YF8	Q93YF8 arabidopsis
23	59.5	35.2	1084	2 Q48947	Q48947 arabidopsis
24	59.5	35.2	1088	2 Q9SJ22	Q9SJ22 arabidopsis
25	59	34.9	97	2 Q6V9B5	Q6V9B5 brachydanio
26	59	34.9	97	2 AAQ24225	AAQ24225 brachydanio
27	57.5	34.0	192	2 Q707H1	Q707H1 escherichia
28	57.5	34.0	192	2 CAE85184	CAE85184 escherich
29	57.5	34.0	192	2 Q7C009	Q7C009 shigella fl
30	57.5	34.0	199	2 Q83J00	Q83J00 shigella fl
31	57.5	34.0	199	2 Q8PKT6	Q8PKT6 escherichia

32	57.5	34.0	1078	2 Q6UPF1	Q6UPF1 zea mays (m
33	57.5	34.0	1078	2 AAR23310	AAR23310 zea mays
34	57.5	34.0	1084	2 Q6GUG6	Q6GUG6 pinus radia
35	57	33.7	99	2 Q8AV10	Q8AV10 brachydanio
36	57	33.7	99	2 AAS92649	AAS92649 brachydanio
37	57	33.7	424	2 Q9VCS4	Q9VCS4 drosophila
38	56.5	33.4	293	2 Q7VB23	Q7VB23 prochloroco
39	56.5	33.4	346	2 Q8L778	Q8L778 arabidopsis
40	56.5	33.4	366	2 Q94U06	Q94U06 arabidopsis
41	56.5	33.4	1069	2 Q9F1B9	Q9F1B9 arabidopsis
42	56.5	33.4	1081	2 Q65338	Q65338 arabidopsis
43	56.5	33.4	1084	2 Q9FCF9	Q9FCF9 arabidopsis
44	56.5	33.4	1087	2 Q6XZC2	Q6XZC2 populus tre
45	56.5	33.4	1087	2 AAP40636	AAP40636 populus t

ALIGNMENTS

RESULT 1	SDF1_MOUSE	STANDARD;	PRT;	89 AA.
AC	P40224;			
DT	01-FEB-1995 (Rel. 31, Created)			
DT	01-FEB-1995 (Rel. 31, Last sequence update)			
DT	01-OCT-2004 (Rel. 45, Last annotation update)			
DE	Stromal cell-derived factor 1 precursor (SDF-1) (CXCL12) (Pre-B cell growth stimulating factor) (PBSF) (12-O-tetradecanoylphorbol 13-acetate repressed protein 1) (TPAR1) (Thymic lymphoma cell stimulating factor) (TISF).			
DE	factor) (TISF).			
GN	Name=Cxcl12; Synonyms=Sdf1;			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=94181581; PubMed=8134392;			
RA	Nagasawa T., Kikutani H., Kishimoto T.;			
RT	"Molecular cloning and structure of a pre-B-cell growth-stimulating factor.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 91:2305-2309(1994).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=93342488; PubMed=8342023;			
RA	Taahiro K., Tada H., Heilker R., Shirozu M., Nakano T., Honjo T.;			
RT	"Signal sequence trap: a cloning strategy for secreted proteins and type I membrane proteins.";			
RL	Science 261:600-603(1993).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=95073497; PubMed=7982471;			
RA	Jiang W., Zhou P., Kahn S.M., Tomita N., Johnson M.D., Weinstein I.B.;			
RT	"Molecular cloning of TPARI, a gene whose expression is repressed by the tumor promoter 12-O-tetradecanoylphorbol 13-acetate (TPA).";			
RL	Exp. Cell Res. 215:284-293(1994).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RX	STRAIN=AKR/J;			
RA	Nomura M., Nakata Y., Uzawa A., Nose M., Akashi M., Suzuki G.;			
RT	Submitted (DEC-1994) to the EMBL/GenBank/DBJ databases.			
RN	[5]			
RP	SEQUENCE FROM N.A. (ISOFORM ALPHA).			
RX	STRAIN=C57BL/6J; TISSUE=Kidney;			
RA	MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;			
RT	Ozekati Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.;			
RL	Nakada I., Oseko N., Saito R., Suzuki H., Yamanka I., Kiyosawa H.,			
RA	Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gotohori T.,			
RA	Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,			
RA	Schirral L.M., Kanapin A., Matsuda H., Batalov S., Betsel K.W.,			
RA	Blake J.B., Bradt D., Brusic V., Chochia C., Corbani L.E., Cousins S.,			
RA	Dalla B., Dregani T.A., Fletcher C.F., Forrest A., Frazer K.S.,			
RA	Gasterland T., Gariboldi M., Giasi C., Godzik A., Gough J.,			

RA Grimmond S., Guetlich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawai H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konegaya A., Kurochko I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numa K., Okido T., Pavan W.J., Pettea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.V., Qi D., Ramachandran S.,
RA Ravelet J.C., Reed D.J., Reid J., Ring B., Ringwald M.,
RA Sanderlin A., Schneider C., Sempile C.A., Setou M., Shitama K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Vercaro R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilmig L.G., Wyszynski-Boris A., Yangisawa M., Yang I., Yang L.,
RA Yuan Z., Zavalan M., Zhu Y., Zimmer A., Zimnicki P., Hayatsu N.,
RA Hironaka-Kishikawa T., Kono H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shiragawa A.,
RA Yamanishi A., Yoshino M., Waterson R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.,
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs."
RL Nature 420:563-573(2002).
RN [6]
RP SEQUENCE FROM N.A. (ISOFORM ALPHA).
RC STRAIN=CS7BL/6J; TISSUE=Mammary gland;
RX MEDLINE=23388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strauberg R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Kleiener R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Datcenco L., Maruina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scalapino M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedini T.B., Toshiyuki S., Carninci P., Prange C.,
RA Bates S.S., Loguallano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bock S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hilyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Buttefield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
RA Scherch A., Schein J.B., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -1- FUNCTION: Chemottractant active on T-lymphocytes, monocytes, but
CC not neutrophils.
CC -1- FUNCTION: Stimulates the proliferation of bone marrow-derived b
CC progenitor cells in the presence of IL-7 as well as growth of the
CC stromal cell-dependent B-cell clone DM34 cells.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named Isoform=2;
CC Name=Alpha;
CC IsoId=P40224-1; Sequence=Displayed;
CC Name=Beta;
CC IsoId=P40224-2; Sequence=VSP_001057;
CC -1- SIMILARITY: Belongs to the Interleukin alpha (chemokine CXC)
CC family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.ebi.ac.uk/announcements>
CC or send an email to license@ebi.ac.uk).
CC -----
CC EMBL; D21072; BAA04648.1; -
CC EMBL; L12029; AAA040100.1; -
CC EMBL; L12030; AAA040101.1; -
CC EMBL; S74318; AAB32650.1; -
CC EMBL; D43804; BAA07862.1; -

DR EMBL; D43805; BAA07863.1; -
DR EMBL; AK075596; BAC35845.1; -
DR EMBL; BC006640; AAB06640.1; -
DR FTR; A53497; A53497.
DR FTR; 181182; 181182.
DR HSSP; P48061; 1SDP.
DR MGI; MGI:103556; Cxcl12.
DR GO; GO:0008009; F:chemokine activity; IDA.
DR GO; GO:0007420; P:brain development; IDA.
DR GO; GO:0030334; P:regulation of cell migration; IDA.
DR GO; GO:0042098; P:T-cell proliferation; IMP.
DR InterPro; IPR002473; C-X-C/Interlkn.8.
DR InterPro; IPR001811; Chemokine IL8.
DR InterPro; IPR001089; CXC_chemkine_sm1.
DR Pfam; PF00048; IL8; 1.
DR PRINTS; PR00436; INTERLEUKIN8.
DR PROSITE; PS00471; SMALL_CYTOKINES_CXC; FALSE NEG.
DR ALTERNATIVE SPLICING: Chemotaxis; Cytokine; Growth factor; Signal.
KW SIGNAL
FT CHAIN 1 21 potential.
FT DISULFID 30 55 By similarity.
FT DISULFID 32 71 By similarity.
FT VARSPIC 89 89 K->KRLK (in isoform Beta).
FT FTID=VSP_001057.
SQ SEQUENCE 89 AA; 10032 MW; C48BAD69078B55FA CRC64;
Query Match 70.1%; Score 118.5; DB 1; Length 89;
Best Local Similarity 40.3%; Pred. No. 1.3e-09;
Matches 27; Conservative 0; Mismatches 3; Indels 37; Gaps 1;
QY 1 KPVSLSYRCRCRFFGG-----GLKRIQE 23
DB 22 KPVSLSYRCRCRFFGSHIRANVYKHLKILNTPCALQIVARLKNRRQVCIDPKLWIOE 81
QY 24 YLEKALN 30
DB 82 YLEKALN 88
RESULT 2
QY 08HYPO PRELIMINARY; PRT; 89 AA.
AC 08HYPO;
DT 01-MAR-2003 (TEMBREL. 23, Created)
DT 01-MAR-2003 (TEMBREL. 23, Last sequence update)
DT 01-JUN-2003 (TEMBREL. 24, Last annotation update)
DE Chemokine CXCL12/SDF-1ALPHA.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22123042; PubMed=12126650;
RA Basu S., Schaefer T.M., Ghosh M., Fuller C.L., Reinhart T.A.,
RT "Molecular cloning and sequencing of 25 different rhesus macaque
RT chemokine cDNAs reveals evolutionary conservation among C, CC, CXC,
RT AND CXC families of chemokines."
RL Cytokine 18:140-148(2002).
DR EMBL; AF49283; AAN76086.1; -
DR HSSP; P48061; 1SDP.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0008009; F:chemokine activity; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR002473; C-X-C/Interlkn.8.
DR InterPro; IPR001811; Chemokine IL8.
DR Pfam; PF00048; IL8; 1.
DR PRINTS; PR00436; INTERLEUKIN8.
DR SMART; SM00199; SCY; 1.
SQ SEQUENCE 89 AA; 10105 MW; AD531633C6DC2B07 CRC64;
Query Match 70.1%; Score 118.5; DB 2; Length 89;

Best Local Similarity 40.3%; Pred. No. 1.3e-09;
Matches 27; Conservative 0; Mismatches 3; Indels 37; Gaps 1;

Qy 1 KPVSLSYRCPCRFPGG-----GLKWIQE 23
|||
22 KPVSLSYRCPCRFPGSHVAVANVHLKILNTPNCALQIVARLKNNNRQVCIDPRLKWIQE 81
|||

Db 24 YLEKALN 30
|||
82 YLEKALN 88

RESULT 3

ID BAA28601 PRELIMINARY; PRT; 89 AA.

AC BAA28601;
DT 02-MAR-2004 (TREMBlrel. 27, Created)
DT 02-MAR-2004 (TREMBlrel. 27, Last sequence update)
DT 02-MAR-2004 (TREMBlrel. 27, Last annotation update)
DE Stromal cell-derived factor-1 a precursor.

GN SDF-1a.
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;

RN [1]
RP SEQUENCE FROM N.A.

RC TISSUE=thymus;

RA Sato B., Kohmoto M., Mikami T.;

RT "Molecular cloning and sequencing of feline stromal cell-derived

factor-1 a and b.";

RL Eur. J. Immunogenet. 0:0-0(1998).

DR EMBL; AB011965; BAA28601.1;

FT SIGNAL 1 18 POTENTIAL.

FT CHAIN 19 89 STROMAL CELL-DERIVED FACTOR-1A.

SO SEQUENCE 89 AA; 10018 MW; 81E9BB373B2F85FD CRC64;

Qy 1 KPVSLSYRCPCRFPGG-----GLKWIQE 23
|||

Db 22 KPVSLSYRCPCRFPGSHVAVANVHLKILNTPNCALQIVARLKNNNRQVCIDPRLKWIQE 81
|||

Qy 24 YLEKALN 30
|||

Db 82 YLEKALN 88

Qy 1 KPVSLSYRCPCRFPGG-----GLKWIQE 23
|||

Db 22 KPVSLSYRCPCRFPGSHVAVANVHLKILNTPNCALQIVARLKNNNRQVCIDPRLKWIQE 81
|||

Qy 24 YLEKALN 30
|||

Db 82 YLEKALN 88

Qy 1 KPVSLSYRCPCRFPGG-----GLKWIQE 23
|||

Db 22 KPVSLSYRCPCRFPGSHVAVANVHLKILNTPNCALQIVARLKNNNRQVCIDPRLKWIQE 81
|||

Qy 24 YLEKALN 30
|||

Db 82 YLEKALN 88

Qy 1 KPVSLSYRCPCRFPGG-----GLKWIQE 23
|||

Db 22 KPVSLSYRCPCRFPGSHVAVANVHLKILNTPNCALQIVARLKNNNRQVCIDPRLKWIQE 81
|||

Qy 24 YLEKALN 30
|||

Db 82 YLEKALN 88

Query Match 70.1%; Score 118.5; DB 2; Length 89;

Best Local Similarity 40.3%; Pred. No. 1.3e-09;
Matches 27; Conservative 0; Mismatches 3; Indels 37; Gaps 1;

Qy 1 KPVSLSYRCPCRFPGG-----GLKWIQE 23
|||
22 KPVSLSYRCPCRFPGSHVAVANVHLKILNTPNCALQIVARLKNNNRQVCIDPRLKWIQE 81
|||

Db 24 YLEKALN 30
|||
82 YLEKALN 88

RESULT 5

ID BAC32216 PRELIMINARY; PRT; 89 AA.

AC BAC32216;
DT 14-APR-2004 (TREMBlrel. 27, Created)
DT 14-APR-2004 (TREMBlrel. 27, Last sequence update)
DT 14-APR-2004 (TREMBlrel. 27, Last annotation update)
DE 9.5 days embryo parthenogenote cDNA, RIKEN full-length enriched

library, clone:8130032A21 product:stromal cell derived factor 1, full
insert sequence.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;

RN [1]
RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Parthenogenote;

RA MEDLINE=22354683; PubMed=12466851;

RT The RIKEN Consortium;

RL the RIKEN Genome Exploration Research Group Phase I & II Team;

RT "Analysis of the mouse transcriptome based on functional annotation of

60,770 full-length cDNAs.";

RL Nature 420:563-573(2002).

RN [2]
RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Parthenogenote;

RA MEDLINE=21085660; PubMed=11217851;

RT RIKEN FANTOM Consortium;

RL "Functional annotation of a full-length mouse cDNA collection.";

RN [3]
RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Parthenogenote;

RA MEDLINE=20493374; PubMed=11042159;

RT Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,

RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;

RT "Normalization and subcloning of cap-trapper-selected cDNAs to

prepare full-length cDNA libraries for rapid discovery of new genes.";

RL Genome Res. 10:1617-1630(2000).

RN [4]
RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Parthenogenote;

RA MEDLINE=20530913; PubMed=11076861;

RT Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,

RA Kono H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,

RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,

RA Yamamoto R., Matsunoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,

RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Watabiki M.,

RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsunura S., Kawai J.,

RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;

RT "RIKEN integrated sequence analysis (RISA) system-384-format

sequencing pipeline with 384 multicapillary sequencer.";

RL Genome Res. 10:1757-1771(2000).

```

RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Parthenogenote;
RA Adachi U., Aizawa K., Akimura T., Atakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hirooka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Kato H., Kawai J., Kohda M., Kondo S., Kono H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohnato N., Okazaki Y.,
RA Saito K., Satoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RA Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AK045092; BAC32216.1; -. CAB8AD69078E55FA CRC64;
SQ SEQUENCE 89 AA; 10032 MW; C4B8AD69078E55FA CRC64;

Query Match 70.1%; Score 118.5; DB 2; Length 89;
Best Local Similarity 40.3%; Pred. No. 1.3e-09;
Matches 27; Conservative 0; Mismatches 3; Indels 37; Gaps 1;

QY 1 KPVSLSYRCPCRFFG-----GLKRIQ 23
    |||||
DB 22 KPVSLSYRCPCRFFESHIRANVHKLINTPNCALQIVARLKNNNQVCIDPKLWIOE 81
    |||||
QY 24 YLEKALN 30
    |||||
DB 82 YLEKALN 88

RESULT 6
BAC35845 PRELIMINARY; PRT; 89 AA.
AC BAC35845;
DT 14-APR-2004 (TrEMBLrel. 27, Created)
DT 14-APR-2004 (TrEMBLrel. 27, Last sequence update)
DE Adult male kidney cDNA, RIKEN full-length enriched library.
DE clone:0610039H13 product:stromal cell derived factor 1, full insert
DE sequence.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Kidney;
RA MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs."
RL Nature 420:563-573(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Kidney;
RA MEDLINE=21085660; PubMed=11217851;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection."
RL Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Kidney;
RA MEDLINE=99279253; PubMed=10349636;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning."
RL Mech. Enzymol. 303:19-44(1999).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Kidney;
RA MEDLINE=20493374; PubMed=11042159;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,

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RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes."
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Kidney;
RA MEDLINE=20530913; PubMed=11076861;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Kono H., Akiyama U., Nishi K., Kusunagi T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsuno K., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Wataniki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsumura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multiplexed capillary sequencer."
RL Genome Res. 10:1757-1771(2000).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Kidney;
RA Adachi U., Aizawa K., Akahira S., Akimura T., Aono H., Arai A.,
RA Atakawa T., Bono H., Carninci P., Fukuda S., Furuno M.,
RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hirooka T., Hori F.,
RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA Kawai J., Kohda M., Kono H., Kouda M., Koya S., Kurihara C.,
RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA Tejima Y., Toya T., Yamamura T., Yamanaka I., Yasunishi A.,
RA Yoshida K., Yoshino M., Muramatsu M., Hayashizaki Y.;
RA Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AK075596; BAC35845.1; -. C4B8AD69078E55FA CRC64;
SQ SEQUENCE 89 AA; 10032 MW; C4B8AD69078E55FA CRC64;

Query Match 70.1%; Score 118.5; DB 2; Length 89;
Best Local Similarity 40.3%; Pred. No. 1.3e-09;
Matches 27; Conservative 0; Mismatches 3; Indels 37; Gaps 1;

QY 1 KPVSLSYRCPCRFFG-----GLKRIQ 23
    |||||
DB 22 KPVSLSYRCPCRFFESHIRANVHKLINTPNCALQIVARLKNNNQVCIDPKLWIOE 81
    |||||
QY 24 YLEKALN 30
    |||||
DB 82 YLEKALN 88

RESULT 7
CAG29279 PRELIMINARY; PRT; 89 AA.
AC CAG29279;
DT 20-MAY-2004 (TrEMBLrel. 27, Created)
DT 20-MAY-2004 (TrEMBLrel. 27, Last sequence update)
DE 20-MAY-2004 (TrEMBLrel. 27, Last annotation update)
DE CXCL12 protein (Fragment).
GN CXCL12
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Ebert L., Schick W., Neubert P., Schatten R., Henze S., Korn B.;
RT "Cloning of human full open reading frames in Gateway(TM) system entry
RT vector (pDONR201)."
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL: CR450283; CAG29279.1; -.
FT NON_TER
FT 89
SQ SEQUENCE 89 AA; 10103 MW; 62B44E8D209C3A14 CRC64;
Query Match 70.1%; Score 118.5; DB 2; Length 89;

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Best Local Similarity 40.3%; Pred. No. 1.3e-09;
Matches 27; Conservative 0; Mismatches 3; Indels 37; Gaps 1;

QY 1 KPVSLSYRCPCRFPGG-----GLKWIQ 23
DB 22 KPVSLSYRCPCRFPGSHVAVANVHKLITNPNCALQIVARLKNRRQVCIDPKLKIQ 81

QY 24 YLEKALN 30
DB 82 YLEKALN 88

RESULT 8

Q9H554 PRELIMINARY; PRT; 92 AA.

AC Q9H554;
DT 01-MAR-2001 (TEMBUREL. 16, Created)
DT 01-MAR-2001 (TEMBUREL. 16, Last sequence update)
DT 01-JUN-2003 (TEMBUREL. 24, Last annotation update)
DE BA20015.1.2 (Stromal cell-derived factor 1, isoform beta)
DE (Fragment).
GN Name=SDP1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OC NCBI_Taxid=9606;
RN (1)
RP SEQUENCE FROM N.A.
RA Bird C.;
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL137026; CAC10202.1; -.
DR HSSP; P48061; ISDF.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0008009; P:immune response; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR002473; C-X-C/Interlkn_8.
DR InterPro; IPR001811; Chemokine_il8.
DR Pfam; PF00048; IL8; 1.
DR PRINTS; PR00436; INTERLEUKIN8.
DR SMART; SM00199; SCY; 1.
FT NON TER 1
SQ SEQUENCE 92 AA; 10510 MW; AEF0C402B48BD20 CRC64;

Query Match 70.1%; Score 118.5; DB 2; Length 92;
Best Local Similarity 40.3%; Pred. No. 1.4e-09;
Matches 27; Conservative 0; Mismatches 3; Indels 37; Gaps 1;

QY 1 KPVSLSYRCPCRFPGG-----GLKWIQ 23
DB 22 KPVSLSYRCPCRFPGSHVAVANVHKLITNPNCALQIVARLKNRRQVCIDPKLKIQ 81

QY 24 YLEKALN 30
DB 82 YLEKALN 88

RESULT 9

SDP1_FELCA STANDARD; PRT; 93 AA.

AC 062657;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Stromal cell-derived factor 1 precursor (SDF-1) (CXCL12).
GN Name=CXCL12; Synonyms=SDP1;
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OC NCBI_Taxid=9685;
RN (1)
RP SEQUENCE FROM N.A. (ISOFORMS ALPHA AND BETA).
RC TISSUE=Thymus;
RX MEDLINE=96450506; PubMed=9777331;

RA Nishimura Y., Miyazawa T., Ikeda Y., Izumiya Y., Nakamura K.,
RA Cai J.S., Sato E., Kohmoto M., Mikami T.;
RT "Molecular cloning and sequencing of feline stromal cell-derived
RT factor-1 alpha and beta."
RL Eur. J. Immunogenet. 25:303-305(1998).
CC -1- FUNCTION: Chemoattractant active on T-lymphocytes, monocytes, but
CC not neutrophils.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=Beta;
CC IsoId=O62657-1; Sequence=Displayed;
CC Name=Alpha;
CC IsoId=O62657-2; Sequence=VSP_001055;
CC -1- SIMILARITY: Belongs to the Interleukin alpha (chemokine CXC)
CC family.

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CC or send an email to license@isb-sib.ch).
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DR EMBL; AB011966; BA28602.1; -.
DR HSSP; P48061; ISDF.
DR InterPro; IPR002473; C-X-C/Interlkn_8.
DR InterPro; IPR001811; Chemokine_il8.
DR InterPro; IPR001089; CXC_chemokine_small.
DR Pfam; PF00048; IL8; 1.
DR PRINTS; PR00436; INTERLEUKIN8.
DR SMART; SM00199; SCY; 1.
DR PROSITE; PS00471; SMALL_CYTOKINES_CXC; FALSE NEG.
KW Alternative splicing; Chemotaxis; Cytokine; Growth factor; Signal.
FT SIGNAL 1
FT CHAIN 22 93 Potential.
FT DISULFID 30 55 By similarity.
FT DISULFID 32 71 By similarity.
FT VARSPIC 90 93 Missing (in isoform Alpha).
FT FTId=VSP_001055.
SQ SEQUENCE 93 AA; 10581 MW; 44FC763711E9BE37 CRC64;

Query Match 70.1%; Score 118.5; DB 1; Length 93;
Best Local Similarity 40.3%; Pred. No. 1.4e-09;
Matches 27; Conservative 0; Mismatches 3; Indels 37; Gaps 1;

QY 1 KPVSLSYRCPCRFPGG-----GLKWIQ 23
DB 22 KPVSLSYRCPCRFPGSHVAVANVHKLITNPNCALQIVARLKNRRQVCIDPKLKIQ 81

QY 24 YLEKALN 30
DB 82 YLEKALN 88

RESULT 10

SDP1_HUMAN STANDARD; PRT; 93 AA.

AC P48061;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE Stromal cell-derived factor 1 precursor (SDF-1) (CXCL12) (pre-B cell
DE growth stimulating factor) (PBSF) (HHRH) [Contains: SDF-1-beta(3-72);
DE SDF-1-alpha(3-67)].
GN Name=CXCL12; Synonyms=SDP1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OC NCBI_Taxid=9606;
RN (1)
RP SEQUENCE FROM N.A.

RA Spotila L.D.;
 RL Submitted (OCT-1994) to the EMBL/GenBank/DBJ databases.
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96039262; PubMed=7490086;
 RA Shitizu M., Nakano T., Inazawa J., Tashiro K., Tada H., Shinohara T.,
 Honjo T.;
 RT "Structure and chromosomal localization of the human stromal cell-
 RT derived factor 1 (SDF1) gene."
 RL Genomics 28:495-500(1995).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM ALPHA).
 RC TISSUE=Liver;
 RA Begum N.A., Barnard G.F.;
 RT "Nucleotide sequence of hRHR, human interferon reduced in hepatomas."
 RL Submitted (JAN-1995) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RX PubMed=15164054; DOI=10.1038/nature02462;
 RA Deloukas P., Eathrowl M.E., Graham D.V., Rubinfeld M., French L.,
 Steward C.A., Sims S.K., Jones M.C., Searle S., Scott C., Howe K.,
 Hunt S.B., Andrews T.D., Gilbert J.G.R., Swarbreck D., Ashurst J.L.,
 Taylor A., Batties J., Bird C.P., Alencough R., Almeida J.P.,
 Banerjee R., Bates K., Beasley H., Bray-Allen S., Brown A.J.,
 Brown J.Y., Burford D.C., Burrill W., Burton J., Cahill P., Camire D.,
 Carter N.P., Chapman J.C., Clark S.Y., Clarke G., Clee C.M., Clegg S.,
 Corby N., Coulson A., Dhani P., Dutta I., Dunn M., Faulkner L.,
 French A., Frankland J.A., Garner P., Garnett J., Grable S.,
 Griffiths C., Grocock R., Gustatson E., Hammond S., Harley J.L.,
 Hart B., Heath P.D., Ho T.P., Hopkins B., Horne J., Howden P.J.,
 Huckle E., Hynds C., Johnson C., Johnson D., Kana A., Kay M.,
 Kimberley A.M., Kirsch J.K., Kokkinaki M., Laird G.K., Lawlor S.,
 Lee H.M., Leongamornlert D.A., Laird G., Lloyd C., Lloyd D.M.,
 Loveland J., Lovell J., McLaren S., McLay K.E., McMurtry A.,
 Mearns-Mohammadi M., Matthews L., Milne S., Nickerson T.,
 Nguyen M., Overton-Latty E., Palmer S.A., Pearce A.V., Beck A.I.,
 Peltan S., Phillips B., Porter K., Rice C.M., Rogosin A., Rose M.T.,
 Sarrafidou T., Shira H.K., Showkhen R., Skuce C.D., Smith M.,
 Strachan L., Sycamore N., Tester J., Thorpe A., Torcaso W.,
 Tracey A., Tromans A., Tsolas J., Wall M., Walsh J., Wang H.,
 Weinlock K., West A.P., Willey D.L., Whitehead S.L., Wilming L.,
 Wray P.W., Young L., Chen Y., Lovering R.C., Moschonas N.K.,
 Stebert R., Fichtel K., Bentley D., Durbin R., Hubbard T.,
 Doucette-Stamm L., Beck S., Smith D.R., Rogers J.;
 RT "The DNA sequence and comparative analysis of human chromosome 10."
 RL Nature 429:375-381(2004).
 RN [5]
 RP SEQUENCE FROM N.A. (ISOFORM ALPHA).
 RC TISSUE=Brain;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 Altschul S.F., Zeeberg B., Blencow K.H., Scheetor C.F., Bhat N.K.,
 Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 Diachenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,
 Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Pierce T.E.,
 Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Scheer T.E.,
 Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hultk S.W.,
 Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 Butterfield Y.S.N., Krzywinski M.I., Skalek U., Smalene D.E.,
 Scherch A., Schein J.E., Jones S.J.M., Matra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RP IDENTIFICATION OF SDF-1ALPHA(3-67) AND SDF-1BETA(3-72) BY MASS

RP SPECTROMETRY, AND N-TERMINAL AND C-TERMINAL PROCESSING.
 RX PubMed=14525775; DOI=10.1182/blood-2003-08-2857;
 RA De la Luz Sierra M., Yang F., Narazaki M., Salvucci O., Davis D.,
 Yarchean R., Zhang H.H., Fales H., Toesio G.;
 RT "Differential processing of stromal-derived factor-1alpha and beta
 RT explains functional diversity."
 RL Blood 103:2452-2459(2004).
 RN [7]
 RP STRUCTURE BY NMR OF 22-88.
 RX MEDLINE=96046030; PubMed=9384579;
 RA Crump M.P., Gong Y.H., Loetscher P., Rajaratnam K., Amara A.,
 Arenzana-Seisdedos F., Vitellizier J.L., Baggiolini M., Sykes B.D.,
 Clark-Lewis I.;
 RT "Solution structure and basis for functional activity of stromal cell-
 RT derived factor-1; dissociation of CXCR4 activation from binding and
 RT inhibition of HIV-1."
 RL EMBO J. 16:6996-7007(1997).
 RN [8]
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 22-88.
 RX MEDLINE=98284037; PubMed=9618518;
 RA Dealwis C., Fernandez E.J., Thompson D.A., Simon R.J., Slani M.A.,
 La Lio E.;
 RT "Crystal structure of chemically synthesized [N3A] stromal cell-
 RT derived factor 1alpha, a potent ligand for the HIV-1 'Fusin'
 RT coreceptor."
 RL Proc. Natl. Acad. Sci. U.S.A. 95:6941-6946(1998).
 CC -1- FUNCTION: Chemotactant active on T-lymphocytes, monocytes, but
 CC not neutrophils. SDF-1-beta(3-72) and SDF-1-alpha(3-67) show a
 CC reduced chemotactic activity. Binding to cell surface
 CC proteoglycans seems to inhibit formation of SDF-1-alpha(3-67) and
 CC thus to preserve activity on local sites.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=Beta; Synonyms=SDF-1-beta(1-72);
 CC IsoId=IP48061-1; Sequence=Displayed;
 CC Name=Alpha; Synonyms=SDF-1-alpha(1-68);
 CC IsoId=IP48061-2; Sequence=VSP 001056;
 CC -1- PTM: Processed form SDF-1beta(3-72) and SDF-1alpha(3-67) are
 CC produced after secretion by proteolytic cleavage of isoforms Beta
 CC and Alpha, respectively. The N-terminal processing is probably
 CC achieved by DPP4. Isoform Alpha is first cleaved at the C-terminus
 CC to yield a SDF-1-alpha(1-67) intermediate before being processed
 CC at the N-terminus. The C-terminal processing of isoform Alpha is
 CC reduced by binding to heparin and, probably, cell surface
 CC proteoglycans.
 CC -1- SIMILARITY: Belongs to the Interferon alpha (chemokine Cxk)
 CC family.
 CC -----
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 CC -----
 CC EMBL: U16753; AAA97434.1; -;
 CC EMBL: I36033; AAB39332.1; -;
 CC EMBL: I36034; AAB39333.1; -;
 CC EMBL: U19495; AAB40516.1; -;
 CC EMBL: AL137026; CAC10203.1; -;
 CC EMBL: BC039893; AAH39893.1; -;
 CC PIR: G01540; G01540.
 CC PDB: 1A15; X-ray; A/B=22-88.
 CC PDB: 1QG7; X-ray; A/B=22-88.
 CC PDB: 1SDP; NMR; @=22-88.
 CC PDB: 2SDP; NMR; @=22-88.
 CC Genew; HGNC:10672; CXCL12.
 CC MIM: 600835; -;
 CC GO: GO:0008009; Chemokine activity; TAS.
 CC GO: GO:0005102; Receptor binding; TAS.
 CC GO: GO:0006874; Picalcium ion homeostasis; TAS.

```

DR GO: GO:0007155; P:cell adhesion; TAS.
DR GO: GO:0006935; P:chemotaxis; TAS.
DR GO: GO:0008015; P:circulation; TAS.
DR GO: GO:0007186; P:G-protein coupled receptor protein signalin. . .; TAS.
DR GO: GO:0006955; P:immune response; TAS.
DR GO: GO:0008064; P:regulation of actin polymerization and/or d. . .; TAS.
DR GO: GO:0009615; P:response to virus; TAS.
DR GO: GO:0007165; P:signal transduction; TAS.
DR InterPro: IPR002473; C-X-C/Interlkn_8.
DR InterPro: IPR001811; Chemokine_118.
DR InterPro: IPR001089; CXC_chkline_small.
DR Pfam: PF00048; IL8_1.
DR PRINTS: PR00436; INTERLEUKINE.
DR PROSITE: PS00471; SMALL_CITOKINES_CXC; FALSE_NEG.
KW 3D-structure; Alternative splicing; Chemotaxis; Cytokine;
KW Growth factor; Signal.
FT SIGNAL 1 21 Potential.
FT CHAIN 22 93 Stromal cell-derived factor 1.
FT CHAIN 24 93 SDF-1beta(3-72).
FT CHAIN 24 88 SDF-1alpha(3-67).
FT DISULFID 30 55
FT DISULFID 32 71
FT VARSPPLIC 90 93 Missing (in isoform Alpha).
FT STRAND 36 36 /FTId=VSP_001056.
FT HELIX 41 43
FT STRAND 44 50
FT TURN 53 54
FT STRAND 59 63
FT TURN 64 66
FT STRAND 69 72
FT TURN 74 75
FT HELIX 77 82
FT TURN 83 83
FT HELIX 84 87
SQ SEQUENCE 93 AA; 10666 MW; 505B5A29C2B44E8D CRC64;

Query Match 70.1%; Score 118.5; DB 1; Length 93;
Best Local Similarity 40.3%; Pred. No. 1.4e-09;
Matches 27; Conservative 0; Mismatches 3; Indels 37; Gaps 1;

Qy 1 KPVSLSYRCPCRFPGG-----GLKNVIOE 23
Db 22 KPVSLSYRCPCRFPGSHVAVRANVKKILNTPNCALQIVARLKNNRQVCIDPKLKIIOE 81
Qy 24 YLEKALN 30
Db 82 YLEKALN 88

RESULT 11
Q6EKW4 PRELIMINARY; PRT; 116 AA.
ID O6EKW4
AC O6EKW4
DT 01-OCT-2004 (TREMBlrel. 28, Created)
DT 01-OCT-2004 (TREMBlrel. 28, Last sequence update)
DT 01-OCT-2004 (TREMBlrel. 28, Last annotation update)
DE CXC12 chemokine.
DE Name=CXC12;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OC NCBI_TaxID=9823;
OX RN
RP SEQUENCE FROM N.A.
RX PubMed=15242943;
RA Ledger T.N., Pinton P., Bourges D., Rouni P., Salmon H., Oswald I.P.;
RT "Development of a microarray to specifically analyze immunological
RT gene expression in Swine."
RL Clin. Diagn. Lab. Immunol. 11:691-698(2004).
DR EMBL; AY12066; AAC84094.1; -.
SQ SEQUENCE 116 AA; 12622 MW; 2A1BC0551C2BEAB CRC64;

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Query Match 70.1%; Score 118.5; DB 2; Length 116;
Best Local Similarity 40.3%; Pred. No. 1.7e-09;
Matches 27; Conservative 0; Mismatches 3; Indels 37; Gaps 1;

Qy 1 KPVSLSYRCPCRFPGG-----GLKNVIOE 23
Db 22 KPVSLSYRCPCRFPGSHVAVRANVKKILNTPNCALQIVARLKNNRQVCIDPKLKIIOE 81
Qy 24 YLEKALN 30
Db 82 YLEKALN 88

RESULT 12
Q80ZW4 PRELIMINARY; PRT; 137 AA.
ID Q80ZW4
AC Q80ZW4;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Cxc12 protein.
DE Name=Cxc12;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6; TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan K.C., Moore T., Max S.I., Wang J., Heide F.,
RA Diatchenko L., Marusik A.K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Tohyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mulhally S.J.,
RA Bobak S.A., McEwen P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.U., Huiyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fealey J., Hellton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W., Buttefield Y.S.,
RA Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6; TISSUE=Brain;
RA Strausberg R.;
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC046827; AA046827.1; -.
DR HSSP; P48061; ISDF.
DR MGD; MGI:103556; Cxc12.
DR GO: GO:0008009; P:chemokine activity; IDA.
DR GO: GO:0007420; P:brain development; IDA.
DR GO: GO:0007281; P:germ cell development; IDA.
DR GO: GO:0008354; P:germ cell migration; IDA.
DR GO: GO:0050930; P:induction of positive chemotaxis; IDA.
DR GO: GO:0042098; P:positive regulation of cell migration; IDA.
DR InterPro: IPR002473; C-X-C/Interlkn_8.
DR InterPro: IPR001811; Chemokine_118.
DR Pfam; PF00048; IL8_1.
DR PRINTS; PR00436; INTERLEUKINE8.
DR SMART; SM00199; SCY; 1.
SQ SEQUENCE 137 AA; 15529 MW; 04B47DAB6904DF77 CRC64;

Query Match 70.1%; Score 118.5; DB 2; Length 137;

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Best Local Similarity 40.3%; Pred. No. 2e-09;
Matches 27; Conservative 0; Mismatches 3; Indels 37; Gaps 1;

QY 1 KPVSLSYRCPCRFEGG-----LKWIOE 23
DB 22 KPVSLTYRCPCRFESNVARANIKHLKILSTPNCSLQIVARLKSNSKQVCIDPKLKWIOE 81

QY 24 YLEKALN 30
DB 82 YLEKALN 88

RESULT 13

Q6T7CO PRELIMINARY; PRT; 89 AA.

AC 06T7CO;
DT 05-JUL-2004 (TEMBLrel. 27, Created)
DT 05-JUL-2004 (TEMBLrel. 27, Last sequence update)
DE Stromal cell-derived factor-1 alpha.

OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.

OX NCB1_TaxID=9031;
RN RP SEQUENCE FROM N.A.
RA Raz B., Stebler J.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.

RP TTSUE=SpLeen;
RC Read L.R., Cumberbatch J., Sharif S.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY429472; AAR91695.1; -;
DR EMBL; AY451855; AAR8102.1; -;
DR InterPro; IPR002473; C-X-C/Interlkn_8.
DR InterPro; IPR001811; Chemokine_IL8.
DR Pfam; PF00048; IL8; 1.
DR PRINTS; PR00436; INTERLEUKIN8.
DR SMART; SM00199; SCY; 1.
SQ SEQUENCE 89 AA; 10104 MW; 21E53D121A557965 CRC64;

Query Match 69.5%; Score 117.5; DB 2; Length 89;

Best Local Similarity 38.8%; Pred. No. 1.8e-09;
Matches 26; Conservative 1; Mismatches 3; Indels 37; Gaps 1;

QY 1 KPVSLSYRCPCRFEGG-----LKWIOE 23
DB 22 KPVSLTYRCPCRFESNVARANIKHLKILSTPNCSLQIVARLKSNSKQVCIDPKLKWIOE 81

QY 24 YLEKALN 30
DB 82 YLEKALN 88

RESULT 14

AAR8102 PRELIMINARY; PRT; 89 AA.

AC AAR8102;
DT 02-MAR-2004 (TEMBLrel. 27, Created)
DT 02-MAR-2004 (TEMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TEMBLrel. 27, Last annotation update)
DE Stromal cell derived factor 1.

GN SDF1.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.

OX NCB1_TaxID=9031;
RN RP SEQUENCE FROM N.A.

RC TTSUE=SpLeen;

RA Read L.R., Cumberbatch J., Sharif S.;
RT "Characterization of Chicken SDF-1";
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY451855; AAR8102.1; -;
SQ SEQUENCE 89 AA; 10104 MW; 21E53D121A557965 CRC64;

Query Match 69.5%; Score 117.5; DB 2; Length 89;

Best Local Similarity 38.8%; Pred. No. 1.8e-09;
Matches 26; Conservative 1; Mismatches 3; Indels 37; Gaps 1;

QY 1 KPVSLSYRCPCRFEGG-----LKWIOE 23
DB 22 KPVSLTYRCPCRFESNVARANIKHLKILSTPNCSLQIVARLKSNSKQVCIDPKLKWIOE 81

QY 24 YLEKALN 30
DB 82 YLEKALN 88

RESULT 15

AAR91695 PRELIMINARY; PRT; 89 AA.

AC AAR91695;
DT 14-APR-2004 (TEMBLrel. 27, Created)
DT 14-APR-2004 (TEMBLrel. 27, Last sequence update)
DT 14-APR-2004 (TEMBLrel. 27, Last annotation update)
DE Stromal cell-derived factor-1 alpha.

OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.

OX NCB1_TaxID=9031;
RN RP SEQUENCE FROM N.A.
RA Raz B., Stebler J.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY429472; AAR91695.1; -;
SQ SEQUENCE 89 AA; 10104 MW; 21E53D121A557965 CRC64;

Query Match 69.5%; Score 117.5; DB 2; Length 89;

Best Local Similarity 38.8%; Pred. No. 1.8e-09;
Matches 26; Conservative 1; Mismatches 3; Indels 37; Gaps 1;

QY 1 KPVSLSYRCPCRFEGG-----LKWIOE 23
DB 22 KPVSLTYRCPCRFESNVARANIKHLKILSTPNCSLQIVARLKSNSKQVCIDPKLKWIOE 81

QY 24 YLEKALN 30
DB 82 YLEKALN 88

Search completed: January 4, 2005, 15:49:53
Job time : 61.541 secs